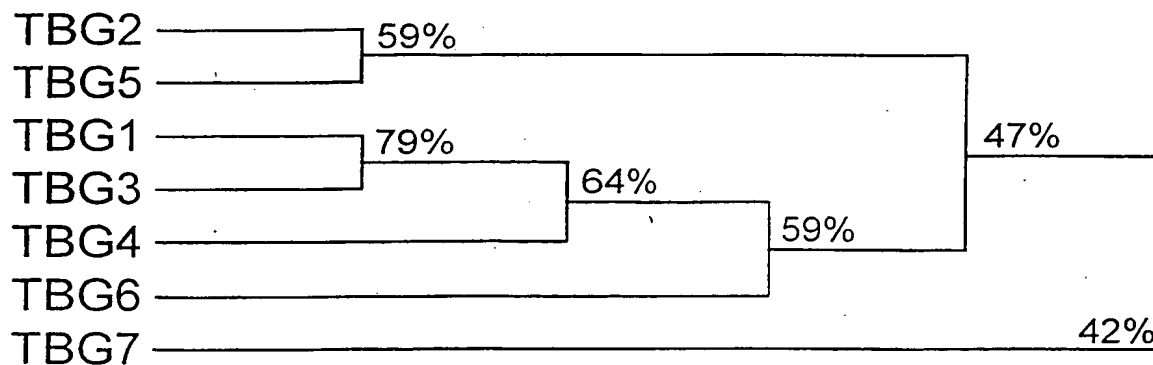


A



B

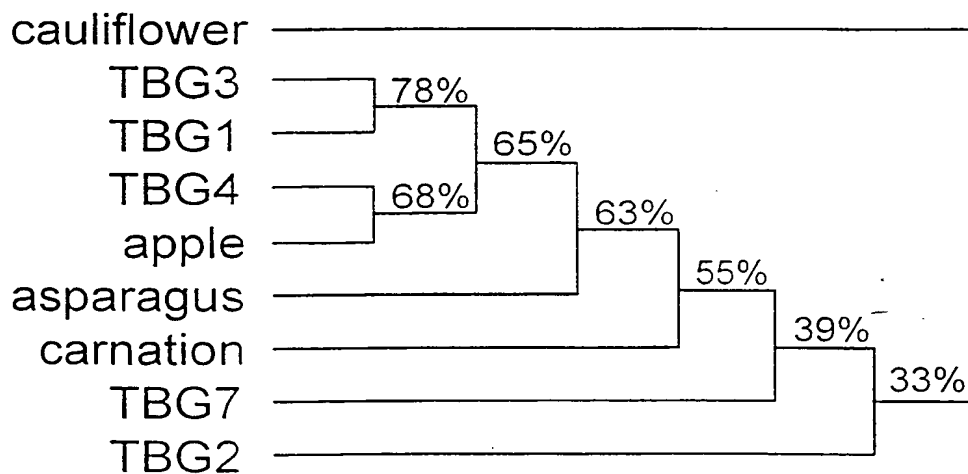


Figure 1. β -Galactosidase phylogenetic tree based on shared amino acid sequence identity. A. Tomato β -galactosidase (TBG) cDNAs. B. Plant β -galactosidases. Higgins-Sharp algorithm (UPGMA method)

Figure 2
Sheet 1 of 12

Gene/clone name: TBG1/pZBG2-1-10; accession number AF023847; Sequence ID number 1

	TTTTTCTTTGTTCTTTTGCTCAGCACTAG	30
31	AGCCTAGAAGAAGGAAAAAAGAAGTATGGACTAATGGAATAAACATAAAAAAGAGAGAAAAAAGAAGAAATCTTCAGACAACA	122
123	AAAACAGCTGTTTTCCCTTCACTACTTTTTTTTTTCCCAATCTCTATATAATTGCAAGAATAGAATAAAGTTGCAACTTGATTAAAAA	214
215	GAAATAAAGCTGTGGGGTAGGGAGGAAGTTAGTTTCATTAGTTTCATTGCTTGTAAAGGCACAATCTTGATTCTTGATTGTTGACAAAT	305
306	ATG GGT TTT TGG ATG GCA ATG TTG CTG ATG TTG TTA TTG TGT TTA TGG GTT TCT TGT GGA ATT GCT TCT	374
1	Met Gly Phe Trp Met Ala Met Leu Leu Met Leu Leu Cys Leu Trp Val Ser Cys Gly Ile Ala Ser	23
375	GTT TCA TAT GAC CAT AAA GCT ATC ATT GTA AAT GGA CAA AGA AAA ATT CTC ATT TCT GGA TCC ATT CAC	443
24	Val Ser Tyr Asp His Lys Ala Ile Ile Val Asn Gly Gln Arg Lys Ile Leu Ile Ser Gly Ser Ile His	46
444	TAC CCT AGA AGC ACC CCT GAG ATG TGG CCA GAT CTT ATT CAG AAG GCA AAA GAA GGG GGA GTT GAT GTT	512
47	Tyr Pro Arg Ser Thr Pro Glu Met Trp Pro Asp Leu Ile Gln Lys Ala Lys Glu Gly Val Asp Val	69
513	ATA CAG ACT TAT GTT TTC TGG AAT GGG CAT GAG CCT GAA GAA GGG AAA TAT TAT TTT GAA GAG AGG TAT	581
70	Ile Gln Thr Tyr Val Phe Trp Asn Gly His Glu Pro Glu Glu Gly Lys Tyr Tyr Phe Glu Glu Arg Tyr	92
582	GAT TTA GTG AAG TTC ATT AAA GTG GTG CAA GAA GCA GGA CTT TAT GTG CAT CTT AGG ATT GGA CCT TAT	650
93	Asp Leu Val Lys Phe Ile Lys Val Val Gln Glu Ala Gly Leu Tyr Val His Leu Arg Ile Gly Pro Tyr	115
651	GCA TGT GCT GAA TGG AAT TTT GGG GGT TTT CCT GTT TGG CTG AAG TAT GTT CCA GGT ATT AGT TTC AGA	719
116	Ala Cys Ala Glu Trp Asn Phe Gly Gly Phe Pro Val Trp Leu Lys Tyr Val Pro Gly Ile Ser Phe Arg	138
720	ACA AAC AAT GAG CCA TTC AAG GCT GCA ATG CAA AAG TTC ACT ACT AAG ATT GTT GAT ATG ATG AAA GCA	788
139	Thr Asn Asn Glu Pro Phe Lys Ala Ala Met Gln Lys Phe Thr Thr Lys Ile Val Asp Met Met Lys Ala	161
789	GAA AAG CTC TAT GAA ACT CAG GGT GGT CCA ATT ATT CTA TCT CAG ATA GAA AAT GAA TAT GGA CCT ATG	857
162	Glu Lys Leu Tyr Glu Thr Gln Gly Gly Pro Ile Ile Leu Ser Gln Ile Glu Asn Glu Tyr Gly Pro Met	184
858	GAG TGG GAA CTA GGT GAA CCT GGT AAA GTT TAC TCA GAA TGG GCA GCC AAA ATG GCT GTG GAT CTT GGC	926
185	Glu Trp Glu Leu Gly Glu Pro Gly Lys Val Tyr Ser Glu Trp Ala Ala Lys Met Ala Val Asp Leu Gly	207
927	ACT GGT GTC CCA TGG ATC ATG TGC AAG CAA GAT GAT GTC CCT GAT CCT ATT ATT AAT ACT TGC AAT GGT	995
208	Thr Gly Val Pro Trp Ile Met Cys Lys Gln Asp Asp Val Pro Asp Pro Ile Ile Asn Thr Cys Asn Gly	230
996	TTC TAC TGT GAC TAC TTC ACA CCA AAT AAG GCT AAT AAA CCC AAG ATG TGG ACT GAA GCC TGG ACA GCC	1064
231	Phe Tyr Cys Asp Tyr Phe Thr Pro Asn Lys Ala Asn Lys Pro Lys Met Trp Thr Glu Ala Trp Thr Ala	253
1065	TGG TTT ACC GAA TTT GGA GGT CCA GTT CCT TAC CGT CCT GCA GAG GAT ATG GCA TTT GCT GTC GCA AGA	1133
254	Trp Phe Thr Glu Phe Gly Gly Pro Val Pro Tyr Arg Pro Ala Glu Asp Met Ala Phe Ala Val Ala Arg	276
1134	TTT ATA CAA ACG GGA GGC TCC TTC ATC AAT TAC TAT ATG TAT CAT GGA GGA ACA AAC TTT GGA AGG ACT	1202
277	Phe Ile Gln Thr Gly Gly Ser Phe Ile Asn Tyr Tyr Met Tyr His Gly Gly Thr Asn Phe Gly Arg Thr	299
1203	TCT GGT GGC CCA TTT ATT GCT ACT AGT TAT GAT TAT GAT GCA CCC CTA GAT GAA TTT GGG TCA TTA CGG	1271
300	Ser Gly Gly Pro Phe Ile Ala Thr Ser Tyr Asp Tyr Asp Ala Pro Leu Asp Glu Phe Gly Ser Leu Arg	322
1272	CAG CCT AAA TGG GGT CAT CTG AAA GAT CTA CAT AGA GCA ATA AAG CTC TGT GAG CCA GCT TTA GTA TCT	1340
323	Gln Pro Lys Trp Gly His Leu Lys Asp Leu His Arg Ala Ile Lys Leu Cys Glu Pro Ala Leu Val Ser	345
1341	GTA GAT CCA ACT GTG ACA TCC TTA GGA AAC TAT CAA GAG GCA CGT GTT TTC AAG TCA GAG TCT GGG GCC	1409
346	Val Asp Pro Thr Val Thr Ser Leu Gly Asn Tyr Gln Glu Ala Arg Val Phe Lys Ser Glu Ser Gly Ala	368
1410	TGC GCT GCC TTC CTA GCA AAT TAC AAC CAG CAC TCT TTT GCT AAA GTG GCA TTT GGG AAC ATG CAT TAT	1478
369	Cys Ala Ala Phe Leu Ala Asn Tyr Asn Gln His Ser Phe Ala Lys Val Ala Phe Gly Asn Met His Tyr	391
1479	AAC TTG CCA CCC TGG TCT ATC AGC ATT CTT CCC GAC TGC AAG AAC ACT GTC TAT AAT ACT GCA AGG GTT	1547
392	Asn Leu Pro Pro Trp Ser Ile Ser Ile Leu Pro Asp Cys Lys Asn Thr Val Tyr Asn Thr Ala Arg Val	414
1548	GGT GCT CAA AGT GCT CAG ATG AAG ATG ACT CCA GTC AGT AGA GGA TTC TCA TGG GAG TCA TTC AAT GAA	1616
415	Gly Ala Gln Ser Ala Gln Met Lys Met Thr Pro Val Ser Arg Gly Phe Ser Trp Glu Ser Phe Asn Glu	437

Sh et 2 of 12
Gene/clone name: TBG1/pZBG2-10; accession number AF023847; Sequence ID number 1 cont.

1617	GAC	GCA	GCA	TCG	CAT	GAA	GAC	GAC	ACT	TTC	ACA	GTT	GTT	GGG	TTA	TTG	GAG	CAG	ATT	AAT	ATC	ACA	AGA	1685
438	Asp	Ala	Ala	Ser	His	Glu	Asp	Asp	Thr	Phe	Thr	Val	Val	Gly	Leu	Leu	Glu	Gln	Ile	Asn	Ile	Thr	Arg	460
1686	GAT	GTA	TCT	GAT	TAC	TTG	TGG	TAT	ATG	ACT	GAC	ATT	GAG	ATT	GAT	CCA	ACA	GAA	GGA	TTT	TTG	AAT	AGT	1754
461	Asp	Val	Ser	Asp	Tyr	Leu	Trp	Tyr	Met	Thr	Asp	Ile	Glu	Ile	Asp	Pro	Thr	Glu	Gly	Phe	Leu	Asn	Ser	483
1755	GGA	AAT	TGG	CCT	TGG	CTT	ACT	GTC	TTT	TCT	GCT	GGC	CAT	GCA	TTG	CAT	GTA	TTC	GTG	AAT	GGT	CAA	TTA	1823
484	Gly	Asn	Trp	Pro	Trp	Leu	Thr	Val	Phe	Ser	Ala	Gly	His	Ala	Leu	His	Val	Phe	Val	Asn	Gly	Gln	Leu	506
1824	GCA	GGA	ACT	GTG	TAC	GGA	AGT	TTA	GAA	AAC	CCA	AAA	CTA	ACT	TTC	AGC	AAC	GGT	ATA	AAT	CTG	AGA	GCT	1892
507	Ala	Gly	Thr	Val	Tyr	Gly	Ser	Leu	Glu	Asn	Pro	Lys	Leu	Thr	Phe	Ser	Asn	Gly	Ile	Asn	Leu	Arg	Ala	529
1893	GGT	GTG	AAC	AAG	ATT	TCT	CTG	CTA	AGC	ATT	GCT	GTT	GGT	CTT	CCG	AAC	GTT	GGC	CCT	CAT	TTT	GAG	ACA	1961
530	Gly	Val	Asn	Lys	Ile	Ser	Leu	Leu	Ser	Ile	Ala	Val	Gly	Leu	Pro	Asn	Val	Gly	Pro	His	Phe	Glu	Thr	552
1962	TGG	AAT	GCT	GGT	GTT	CTT	GGA	CCA	GTT	TCA	CTT	AAT	GGA	CTT	AAT	GAA	GGA	ACA	AGA	GAT	TTA	ACA	TGG	2030
553	Trp	Asn	Ala	Gly	Val	Leu	Gly	Pro	Val	Ser	Leu	Asn	Gly	Leu	Asn	Glu	Gly	Thr	Arg	Asp	Leu	Thr	Trp	575
2031	CAG	AAA	TGG	TTC	TAC	AAG	GTT	GGT	CTA	AAA	GGA	GAA	GCC	CTG	AGT	CTT	CAT	TCA	CTC	AGT	GGT	AGC	CCA	2099
576	Gln	Lys	Trp	Phe	Tyr	Lys	Val	Gly	Leu	Lys	Gly	Glu	Ala	Leu	Ser	Leu	His	Ser	Leu	Ser	Gly	Ser	Pro	598
2100	TCC	GTG	GAG	TGG	GTG	GAA	GGC	TCT	TTA	GTG	GCT	CAG	AAG	CAG	CCA	CTC	AGT	TGG	TAT	AAG	ACT	ACA	TTC	2168
599	Ser	Val	Glu	Trp	Val	Glu	Gly	Ser	Leu	Val	Ala	Gln	Lys	Gln	Pro	Leu	Ser	Trp	Tyr	Lys	Thr	Thr	Phe	621
2169	AAT	GCT	CCA	GAT	GGA	AAT	GAA	CCT	TTG	GCT	TTA	GAT	ATG	AAT	ACC	ATG	GGC	AAA	GGT	CAA	GTA	TGG	ATA	2237
622	Asn	Ala	Pro	Asp	Gly	Asn	Glu	Pro	Leu	Ala	Leu	Asp	Met	Asn	Thr	Met	Gly	Lys	Gly	Gln	Val	Trp	Ile	644
2238	AAT	GGT	CAG	AGC	CTC	GGA	CGC	CAC	TGG	CCT	GCA	TAT	AAA	TCA	TCT	GGA	AGT	TGT	AGT	GTC	TGT	AAC	TAT	2306
645	Asn	Gly	Gln	Ser	Leu	Gly	Arg	His	Trp	Pro	Ala	Tyr	Lys	Ser	Ser	Gly	Ser	Cys	Ser	Val	Cys	Asn	Tyr	667
2307	ACT	GGC	TGG	TTT	GAT	GAG	AAA	AAG	TGC	CTA	ACT	AAC	TGT	GGT	GAG	GGC	TCA	CAA	AGA	TGG	TAC	CAC	GTA	2375
668	Thr	Gly	Trp	Phe	Asp	Glu	Lys	Lys	Cys	Leu	Thr	Asn	Cys	Gly	Glu	Gly	Ser	Gln	Arg	Trp	Tyr	His	Val	690
2376	CCC	CGG	TCT	TGG	CTG	TAT	CCT	ACT	GGA	AAT	TTG	TTA	GTT	GTA	TTC	GAG	GAA	TGG	GGA	GGA	GAT	CCT	TAT	2444
691	Pro	Arg	Ser	Trp	Leu	Tyr	Pro	Thr	Gly	Asn	Leu	Leu	Val	Val	Phe	Glu	Glu	Trp	Gly	Gly	Asp	Pro	Tyr	713
2445	GGA	ATC	ACT	TTA	GTC	AAA	AGA	GAA																

Figure 2

Sheet 3 of 12

Gene/clone name: TBG2/pZBG2-1-12; accession number AF154420; Sequence ID number 2

[illegible]

Figur 2

Sheet 4 of 12

Gene/clone name: TBG2/pZBG2-2; accession number AF154420; Sequence ID number 2 cont.

1383	CTA AAA GCA AGC TCG GAA AGT TTT TCA CAA TCT TGG ATG ACA TTG AAG GAG CCA CTT GGT GTG TGG GGT	1451
461	Leu Lys Ala Ser Ser Glu Ser Phe Ser Gln Ser Trp Met Thr Leu Lys Glu Pro Leu Gly Val Trp Gly	483
1452	GAC AAG AAT TTC ACT TCT AAA GGA ATA CTG GAG CAT CTG AAT GTG ACA AAA GAC CAG TCT GAT TAC CTG	1520
484	Asp Lys Asn Phe Thr Ser Lys Gly Ile Leu Glu His Leu Asn Val Thr Lys Asp Gln Ser Asp Tyr Leu	506
1521	TGG TAT CTG ACC AGG ATA TAT ATT TCT GAT GAT GAC ATC TCA TTT TGG GAG GAA AAT GAT GTT AGT CCA	1589
507	Trp Tyr Leu Thr Arg Ile Tyr Ile Ser Asp Asp Asp Ile Ser Phe Trp Glu Glu Asn Asp Val Ser Pro	529
1590	ACA ATT GAT ATT GAT AGC ATG CGT GAT TTT GTT CGC ATT TTT GTT AAT GGG CAG CTT GCA GGT AGT GTG	1658
530	Thr Ile Asp Ile Asp Ser Met Arg Asp Phe Val Arg Ile Phe Val Asn Gly Gln Leu Ala Gly Ser Val	552
1659	AAA GGC AAA TGG ATC AAG GTG GTT CAA CCT GTT AAG CTG GTT CAG GGA TAC AAC GAC ATA CTG CTA TTA	1727
553	Lys Gly Lys Trp Ile Lys Val Val Gln Pro Val Lys Leu Val Gln Gly Tyr Asn Asp Ile Leu Leu Leu	575
1728	TCT GAG ACG GTG GGA TTG CAG AAT TAT GGT GCC TTC TTG GAG AAG GAT GGG GCA GGT TTT AAA GGT CAG	1796
576	Ser Glu Thr Val Gly Leu Gln Asn Tyr Gly Ala Phe Leu Glu Lys Asp Gly Ala Gly Phe Lys Gly Gln	598
1797	ATA AAG CTT ACA GGA TGC AAA AGC GGG GAT ATC AAT CTC ACA ACA TCT TTA TGG ACC TAC CAG GTG GGG	1865
599	Ile Lys Leu Thr Gly Cys Lys Ser Gly Asp Ile Asn Leu Thr Thr Ser Leu Trp Thr Tyr Gln Val Gly	621
1866	CTT AGA GGC GAA TTC CTG GAA GTA TAT GAT GTC AAT AGT ACT GAA AGT GCA GGA TGG ACT GAG TTT CCC	1934
622	Leu Arg Gly Glu Phe Leu Glu Val Tyr Asp Val Asn Ser Thr Glu Ser Ala Gly Trp Thr Glu Phe Pro	644
1935	ACT GGT ACA ACT CCG TCA GTC TTT TCG TGG TAC AAG ACA AAG TTT GAT GCC CCA GGC GGG ACA GAT CCA	2003
645	Thr Gly Thr Thr Pro Ser Val Phe Ser Trp Tyr Lys Thr Lys Phe Asp Ala Pro Gly Gly Thr Asp Pro	667
2004	GTT GCT CTT GAT TTT AGT AGC ATG GGA AAA GGT CAG GCA TGG GTT AAT GGC CAC CAT GTA GGA AGA TAT	2072
668	Val Ala Leu Asp Phe Ser Ser Met Gly Lys Gly Gln Ala Trp Val Asn Gly His His Val Gly Arg Tyr	690
2073	TGG ACT TTG GTT GCA CCA AAT AAT GGA TGT GGA AGA ACT TGT GAT TAT CGT GGT GCT TAC CAC TCT GAT	2141
691	Trp Thr Leu Val Ala Pro Asn Asn Gly Cys Gly Arg Thr Cys Asp Tyr Arg Gly Ala Tyr His Ser Asp	713
2142	AAA TGT AGG ACA AAC TGT GGA GAG ATT ACT CAG GCC TGG TAC CAT ATA CCT AGA TCA TGG CTA AAG ACA	2210
714	Lys Cys Arg Thr Asn Cys Gly Glu Ile Thr Gln Ala Trp Tyr His Ile Pro Arg Ser Trp Leu Lys Thr	736
2211	TTA AAT AAT GTA CTA GTT ATC TTT GAA GAA ACA GAT AAA ACT CCG TTT GAT ATT TCC ATT TCT ACG CGT	2279
737	Leu Asn Asn Val Leu Val Ile Phe Glu Glu Thr Asp Lys Thr Pro Phe Asp Ile Ser Ile Ser Thr Arg	759
2280	TCT ACT GAA ACC ATT TGT GCT CAA GTA TCG GAA AAG CAC TAT CCA CCT CTA CAT AAG TGG TCT CAT TCG	2348
760	Ser Thr Glu Thr Ile Cys Ala Gln Val Ser Glu Lys His Tyr Pro Pro Leu His Lys Trp Ser His Ser	782
2349	GAG TTT GAC AGA AAG TTG TCT CTG ATG GAT AAA ACA CCA GAA ATG CAC TTG CAG TGT GAC GAA GGA CAT	2417
783	Glu Phe Asp Arg Lys Leu Ser Leu Met Asp Lys Thr Pro Glu Met His Leu Gln Cys Asp Glu Gly His	805
2418	ACA ATC TCT TCT ATT GAA TTT GCA AGC TAT GGA AGT CCG AAT GGC AGC TGT CAA AAG TTC TCA CAA GGA	2486
806	Thr Ile Ser Ser Ile Glu Phe Ala Ser Tyr Gly Ser Pro Asn Gly Ser Cys Gln Lys Phe Ser Gln Gly	828
2487	AAA TGC CAT GCT GCA AAT TCC TTG TCT GTT GTA TCT CAG GCT TGT ATA GGA AGA ACT AGT TGC AGC ATT	2555
829	Lys Cys His Ala Ala Asn Ser Leu Ser Val Val Ser Gln Ala Cys Ile Gly Arg Thr Ser Cys Ser Ile	851
2556	GGC ATT TCC AAT GGT GTA TTT GGA GAT CCA TGT CGA CAC GTT GTG AAG AGT TTG GCT GTT CAA GCA AAA	2624
852	Gly Ile Ser Asn Gly Val Phe Gly Asp Pro Cys Arg His Val Val Lys Ser Leu Ala Val Gln Ala Lys	874
2625	TGC TCA CCA CCA CCA GAC CTC AGC ACT TCA GCT TCC TCG TGA GGAGACTCTGGTAACACGTTAACCTTTTAGAACGAA	2702
875	Cys Ser Pro Pro Pro Asp Leu Ser Thr Ser Ala Ser Ser ...	888
2703	ACGATCCCTTAAAGTCCACTCGTTCCCTCGCCCCGAGCCCTCTGCTACATTTCTCAGATCGCATCGTTACAATCAGGCCGAGAAAAACGTAC	2794
2795	ATGGACGATTTTACTTGTAAATATTTGGTTACTGTATATAAAATGAAAGGAATAATGTTGCTTATGCATATGAGCTGCAAAATTATATGACAA	2886
2887	AGTAACAAATGAAATAGAAAACTCCTGTCTGTCAAAGAATTTTAAACAACACCATTTATTAAAGTTAGTTAATGATTAAAAA	2978
2979	AAAAAA	2984

Figure 2

She 15 of 12

Gene/clone name: TBG3/p2- Oc/bl; accession number AF154421; Sequence ID number 3

1	AGAGTTCATTATTTTTCATTTTGCAATTTTGAAA	30
31	AAGAGGAAAAAATAAGTTAAAGGGGGGGAAAAAGTTTTCATTTTGCCCTTAAAAAGGCACAATCTTGATAGAAAAGGAGATAATTTTAC	121
122	ATG GGT TGT ACG CTT ATA CTA ATG TTG AAT GTG TTG TTG GTG TTG TTG GGT TCA TGG GTT TTT TCT GGA	190
1	Met Gly Cys Thr Leu Ile Leu Met Leu Asn Val Leu Leu Val Leu Leu Gly Ser Trp Val Phe Ser Gly	23
191	ACA GCT TCT GTT TCA TAT GAC CAT AGG GCT ATT ATT GTA AAT GGA CAA AGA AGA ATA CTT ATT TCT GGT	259
24	Thr Ala Ser Val Ser Tyr Asp His Arg Ala Ile Ile Val Asn Gly Gln Arg Arg Ile Leu Ile Ser Gly	46
260	TCT GTT CAT TAT CCA AGA AGC ACT CCT GAG ATG TGG CCA GGT ATT ATT CAA AAG GCT AAA GAA GGA GGT	328
47	Ser Val His Tyr Pro Arg Ser Thr Pro Glu Met Trp Pro Gly Ile Ile Gln Lys Ala Lys Glu Gly Gly	69
329	GTG GAT GTG ATT CAG ACT TAT GTT TTC TGG AAT GGA CAT GAG CCT CAA CAA GGG AAA TAT TAT TTT GAA	397
70	Val Asp Val Ile Gln Thr Tyr Val Phe Trp Asn Gly His Glu Pro Gln Gln Gly Lys Tyr Tyr Phe Glu	92
398	GGG AGA TAT GAT TTA GTG AAG TTT ATT AAG CTG GTG CAC CAA GCA GGA CTT TAT GTC CAT CTT AGA GTT	466
93	Gly Arg Tyr Asp Leu Val Lys Phe Ile Lys Leu Val His Gln Ala Gly Leu Tyr Val His Leu Arg Val	115
467	GGA CCT TAT GCT TGT GCT GAA TGG AAT TTT GGG GGC TTT CCT GTT TGG CTG AAA TAT GTT CCA GGT ATC	535
116	Gly Pro Tyr Ala Cys Ala Glu Trp Asn Phe Gly Gly Phe Pro Val Trp Leu Lys Tyr Val Pro Gly Ile	138
536	AGT TTC AGA ACA GAT AAT GGA CCT TTC AAG GCT GCA ATG CAA AAA TTT ACT GCC AAG ATT GTC AAT ATG	604
139	Ser Phe Arg Thr Asp Asn Gly Pro Phe Lys Ala Ala Met Gln Lys Phe Thr Ala Lys Ile Val Asn Met	161
605	ATG AAA GCG GAA CGT TTG TAT GAA ACT CAA GGG GGG CCA ATA ATT TTA TCT CAG ATT GAG AAT GAA TAT	673
162	Met Lys Ala Glu Arg Leu Tyr Glu Thr Gln Gly Gly Pro Ile Ile Leu Ser Gln Ile Glu Asn Glu Tyr	184
674	GGA CCC ATG GAA TGG GAA CTG GGA GCA CCA GGT AAA TCT TAC GCA CAG TGG GCC GCC AAA ATG GCT GTG	742
185	Gly Pro Met Glu Trp Glu Leu Gly Ala Pro Gly Lys Ser Tyr Ala Gln Trp Ala Ala Lys Met Ala Val	207
743	GGT CTT GAC ACT GGT GTC CCA TGG GTT ATG TGC AAG CAA GAC GAT GCC CCT GAT CCT ATT ATA AAT GCT	811
208	Gly Leu Asp Thr Gly Val Pro Trp Val Met Cys Lys Gln Asp Asp Ala Pro Asp Pro Ile Ile Asn Ala	230
812	TGC AAT GGC TTC TAC TGT GAC TAC TTT TCT CCA AAC AAG GCT TAT AAA CCA AAG ATA TGG ACT GAA GCC	880
231	Cys Asn Gly Phe Tyr Cys Asp Tyr Phe Ser Pro Asn Lys Ala Tyr Lys Pro Lys Ile Trp Thr Glu Ala	253
881	TGG ACT GCA TGG TTT ACT GGT TTT GGA AAT CCA GTT CCT TAC CGT CCT GCT GAG GAC TTG GCA TTT TCT	949
254	Trp Thr Ala Trp Phe Thr Gly Phe Gly Asn Pro Val Pro Tyr Arg Pro Ala Glu Asp Leu Ala Phe Ser	276
950	GTT GCA AAA TTT ATA CAG AAG GGA GGT TCC TTC ATC AAT TAT TAC ATG TAT CAT GGA GGA ACA AAC TTT	1018
277	Val Ala Lys Phe Ile Gln Lys Gly Gly Ser Phe Ile Asn Tyr Tyr Met Tyr His Gly Gly Thr Asn Phe	299
1019	GGA CGG ACT GCT GGT GGT CCA TTT ATT GCT ACT AGT TAT GAC TAT GAT GCA CCA CTT GAT GAA TAT GGA	1087
300	Gly Arg Thr Ala Gly Gly Pro Phe Ile Ala Thr Ser Tyr Asp Tyr Asp Ala Pro Leu Asp Glu Tyr Gly	322
1088	TTA TTG CGA CAA CCA AAA TGG GGT CAC CTG AAA GAT CTG CAT AGA GCA ATA AAG CTT TGT GAA CCA GCT	1156
323	Leu Leu Arg Gln Pro Lys Trp Gly His Leu Lys Asp Leu His Arg Ala Ile Lys Leu Cys Glu Pro Ala	345
1157	TTA GTC TCT GGA GAT CCA GCT GTG ACA GCA CTT GGA CAC CAG CAG GAG GCC CAT GTT TTT AGG TCG AAG	1225
346	Leu Val Ser Gly Asp Pro Ala Val Thr Ala Leu Gly His Gln Gln Glu Ala His Val Phe Arg Ser Lys	368
1226	GCT GGC TCT TGT GCT GCA TTC CTT GCT AAC TAC GAC CAA CAC TCT TTT GCT ACT GTG TCA TTT GCA AAC	1294
369	Ala Gly Ser Cys Ala Ala Phe Leu Ala Asn Tyr Asp Gln His Ser Phe Ala Thr Val Ser Phe Ala Asn	391
1295	AGG CAT TAC AAC TTG CCA CCA TGG TCA ATC AGC ATT CTT CCC GAC TGC AAG AAC ACT GTA TTT AAT ACA	1363
392	Arg His Tyr Asn Leu Pro Pro Trp Ser Ile Ser Ile Leu Pro Asp Cys Lys Asn Thr Val Phe Asn Thr	414
1364	GCA CGG ATC GGT GCT CAA AGT GCT CAG ATG AAG ATG ACT CCA GTC AGC AGA GGA TTG CCC TGG CAG TCA	1432
415	Ala Arg Ile Gly Ala Gln Ser Ala Gln Met Lys Met Thr Pro Val Ser Arg Gly Leu Pro Trp Gln Ser	437
1433	TTC AAT GAA GAG ACA TCA TCT TAT GAA GAC AGT AGT TTT ACA GTT GTT GGG CTA TTG GAA CAG ATA AAT	1501
438	Phe Asn Glu Glu Thr Ser Ser Tyr Glu Asp Ser Ser Phe Thr Val Val Gly Leu Leu Glu Gln Ile Asn	460

0005 0307 0/ 031109 0'008 853



Figure 2
She 16 of 12

Gene/clone name: TB03/p2-1-3/b1; accession number AF154421; Sequence ID number 3 cont.

1502	ACA ACA AGA GAC GTG TCT GAT TAT TTG TGG TAT TCA ACA GAT GTC AAG ATT GAT TCA AGA GAA AAG TTT	1570
461	Thr Thr Arg Asp Val Ser Asp Tyr Leu Trp Tyr Ser Thr Asp Val Lys Ile Asp Ser Arg Glu Lys Phe	483
1571	TTG AGA GGC GGA AAA TGG CCT TGG CTT ACG ATC ATG TCA GCT GGG CAT GCA TTG CAT GTT TTT GTG AAT	1639
484	Leu Arg Gly Gly Lys Trp Pro Trp Leu Thr Ile Met Ser Ala Gly His Ala Leu His Val Phe Val Asn	506
1640	GGT CAA TTA GCA GGA ACT GCA TAT GGA AGT TTA GAA AAA CCG AAA CTA ACT TTC AGT AAA GCC GTA AAT	1708
507	Gly Gln Leu Ala Gly Thr Ala Tyr Gly Ser Leu Glu Lys Pro Lys Leu Thr Phe Ser Lys Ala Val Asn	529
1709	CTG AGA GCA GGT GTT AAC AAG ATT TCT CTA CTG AGC ATT GCT GTT GGC CTT CCG AAT ATC GGC CCA CAT	1777
530	Leu Arg Ala Gly Val Asn Lys Ile Ser Leu Leu Ser Ile Ala Val Gly Leu Pro Asn Ile Gly Pro His	552
1778	TTT GAG ACA TGG AAT GCT GGT GTT CTT GGG CCA GTC TCA CTA ACT GGT CTT GAC GAG GGG AAA AGA GAT	1846
553	Phe Glu Thr Trp Asn Ala Gly Val Leu Gly Pro Val Ser Leu Thr Gly Leu Asp Glu Gly Lys Arg Asp	575
1847	TTA ACA TGG CAG AAA TGG TCT TAC AAG GTT GGT CTA AAA GGA GAA GCC TTG AGC CTC CAT TCA CTC AGT	1915
576	Leu Thr Trp Gln Lys Trp Ser Tyr Lys Val Gly Leu Lys Gly Glu Ala Leu Ser Leu His Ser Leu Ser	598
1916	GGT AGC TCG TCA GTT GAG TGG GTC GAG GGT TCT TTA GTG GCT CAG AGA CAG CCA CTC ACA TGG TAC AAG	1984
599	Gly Ser Ser Ser Val Glu Trp Val Glu Gly Ser Leu Val Ala Gln Arg Gln Pro Leu Thr Trp Tyr Lys	621
1985	AGC ACT TTT AAT GCT CCA GCT GGA AAT GAT CCT TTG GCT TTA GAC TTG AAT ACC ATG GGC AAA GGA CAA	2053
622	Ser Thr Phe Asn Ala Pro Ala Gly Asn Asp Pro Leu Ala Leu Asp Leu Asn Thr Met Gly Lys Gly Gln	644
2054	GTG TGG ATA AAT GGT CAA AGC CTC GGA CGC TAT TGG CCT GGA TAT AAA GCA TCT GGT AAC TGC GGT GCC	2122
645	Val Trp Ile Asn Gly Gln Ser Leu Gly Arg Tyr Trp Pro Gly Tyr Lys Ala Ser Gly Asn Cys Gly Ala	667
2123	TGT AAC TAT GCA GGC TGG TTT AAT GAG AAA AAA TGC CTA AGT AAC TGT GGA GAG GCT TCA CAA CGA TGG	2191
668	Cys Asn Tyr Ala Gly Trp Phe Asn Glu Lys Lys Cys Leu Ser Asn Cys Gly Glu Ala Ser Gln Arg Trp	690
2192	TAT CAT GTT CCC CGT TCT TGG CTG TAT CCT ACT GGA AAT TTG TTA GTT CTA TTT GAG GAA TGG GGA GGA	2260
691	Tyr His Val Pro Arg Ser Trp Leu Tyr Pro Thr Gly Asn Leu Leu Val Leu Phe Glu Glu Trp Gly Gly	713
2261	GAG CCT CAT GGA ATC TCT TTG GTA AAA AGA GAA GTT GCA AGT GTT TGT GCA GAT ATA AAC GAA TGG CAA	2329
714	Glu Pro His Gly Ile Ser Leu Val Lys Arg Glu Val Ala Ser Val Cys Ala Asp Ile Asn Glu Trp Gln	736
2330	CCA CAG TTG GTG AAT TGG CAA ATG CAA GCA TCT GGT AAA GTT GAC AAA CCA CTG AGA CCT AAA GCT CAC	2398
737	Pro Gln Leu Val Asn Trp Gln Met Gln Ala Ser Gly Lys Val Asp Lys Pro Leu Arg Pro Lys Ala His	759
2399	CTC TCG TGT GCT TCT GGT CAG AAG ATT ACT TCA ATC AAA TTT GCA AGC TTT GGA ACA CCA CAA GGG GTC	2467
760	Leu Ser Cys Ala Ser Gly Gln Lys Ile Thr Ser Ile Lys Phe Ala Ser Phe Gly Thr Pro Gln Gly Val	782
2468	TGC GGA AGC TTC CGT GAA GGA AGC TGC CAC GCC TTC CAC TCA TAT GAT GCT TTT GAA AGG TAT TGC ATC	2536
783	Cys Gly Ser Phe Arg Glu Gly Ser Cys His Ala Phe His Ser Tyr Asp Ala Phe Glu Arg Tyr Cys Ile	805
2537	GGG CAA AAC TCG TGC TCA GTA CCT GTA ACA CCA GAG ATC TTT GGA GGT GAT CCA TGT CCA CAT GTT ATG	2605
806	Gly Gln Asn Ser Cys Ser Val Pro Val Thr Pro Glu Ile Phe Gly Gly Asp Pro Cys Pro His Val Met	828
2606	AAG AAA CTC TCA GTT GAG GTT ATT TGC AGT TGA TGACACTGAGGAGAAACAAATAAAAGTGGTTTCAGTTAGTTGTCTGAA	2686
829	Lys Lys Leu Ser Val Glu Val Ile Cys Ser ***	840
2687	CATATCAAAAAGTTGGCTTTGATGGAGGTGAAGTTGTACAGATATGCAACACACCTTTCCATTTGAGGCACATATGAATTGCAATGGCCCAA	2778
2779	GATTCGTACATATATGTTGGTTACTGTCAAGTTGGTATTGGTTTGCAAAATGTAACACAGTAGTATAGTCATTGGTTCAAGTGCCGATCGAG	2870
2871	ATTGTGCTAGTGGGAGTAGTAGGTACCGATCGATCTATCGTTGTTTGCAAAAGCTGGCCCTAGATTCCACTATTATTATAACAAAGAAAGC	2962
2963	ACAATGAGACTGATTCTTGATTAGTCCATGTGTAGATATTGTTACTGTTGGAATTTGCAAAATCTTGTGATTTTCAGCAAAAAAAAAAAAAA	3054
3055	AAAAAAAAAAAAAA	3069

Figure 2
Sheet 7 of 12one/clone name: TBG4/pZBG2-~~1~~pTombgal4; accession number AF02035 Sequence ID number 4

1	AAAAAAGTTTCAATTTTTTCTAAAATAAAAAAAATTCATTTTTTTGAATGTGGAAAAA	63
64	ATG CTA AGG ACT AAT GTG TTG TTG TTA TTA GTT ATT TGT TTA TTG GAT TTT TTT TCT TCA GTG AAA GCT	132
1	Met Leu Arg Thr Asn Val Leu Leu Leu Val Ile Cys Leu Leu Asp Phe Phe Ser Ser Val Lys Ala	23
133	AGT GTT TCT TAT GAT GAC AGA GCT ATA ATC ATA AAT GGG AAA AGA AAA ATT CTT ATT TCT GGT TCA ATT	201
24	Ser Val Ser Tyr Asp Asp Arg Ala Ile Ile Ile Asn Gly Lys Arg Lys Ile Leu Ile Ser Gly Ser Ile	46
202	CAT TAT CCA AGA AGC ACT CCA CAG ATG TGG CCT GAT CTT ATA CAA AAG GCT AAA GAT GGA GGC TTA GAT	270
47	His Tyr Pro Arg Ser Thr Pro Gln Met Trp Pro Asp Leu Ile Gln Lys Ala Lys Asp Gly Gly Leu Asp	69
271	GTT ATT GAA ACT TAT GTT TTC TGG AAT GGA CAT GAG CCT TCT CCT GGA AAA TAT AAT TTT GAA GGA AGA	339
70	Val Ile Glu Thr Tyr Val Phe Trp Asn Gly His Glu Pro Ser Pro Gly Lys Tyr Asn Phe Glu Gly Arg	92
340	TAT GAT CTT GTT AGA TTC ATC AAA ATG GTA CAA AGA GCA GGA CTT TAT GTC AAT TTA CGT ATT GGC CCT	408
93	Tyr Asp Leu Val Arg Phe Ile Lys Met Val Gln Arg Ala Gly Leu Tyr Val Asn Leu Arg Ile Gly Pro	115
409	TAC GTC TGT GCT GAA TGG AAC TTT GGG GGA TTC CCT GTT TGG CTA AAA TAT GTG CCT GGT ATG GAA TTT	477
116	Tyr Val Cys Ala Glu Trp Asn Phe Gly Gly Phe Pro Val Trp Leu Lys Tyr Val Pro Gly Met Glu Phe	138
478	AGA ACA AAC AAT CAG CCT TTT AAG GTG GCT ATG CAA GGA TTT GTT CAG AAA ATA GTC AAC ATG ATG AAG	546
139	Arg Thr Asn Asn Gln Pro Phe Lys Val Ala Met Gln Gly Phe Val Gln Lys Ile Val Asn Met Met Lys	161
547	TCA GAA AAT TTG TTT GAA TCT CAA GGA GGA CCA ATA ATT ATG GCC CAG ATA GAA AAT GAG TAT GGA CCA	615
162	Ser Glu Asn Leu Phe Glu Ser Gln Gly Gly Pro Ile Ile Met Ala Gln Ile Glu Asn Glu Tyr Gly Pro	184
616	GTA GAA TGG GAA ATT GGT GCT CCT GGT AAA GCT TAT ACA AAA TGG GCA GCT CAA ATG GCT GTA GGT TTG	684
185	Val Glu Trp Glu Ile Gly Ala Pro Gly Lys Ala Tyr Thr Lys Trp Ala Ala Gln Met Ala Val Gly Leu	207
685	AAA ACT GGT GTC CCA TGG ATC ATG TGT AAG CAA GAG GAT GCT CCT GAT CCT GTG ATT GAT ACT TGT AAT	753
208	Lys Thr Gly Val Pro Trp Ile Met Cys Lys Gln Glu Asp Ala Pro Asp Pro Val Ile Asp Thr Cys Asn	230
754	GGC TTC TAC TGC GAA GGG TTC CGT CCT AAT AAG CCT TAC AAA CCT AAA ATG TGG ACA GAA GTA TGG ACT	822
231	Gly Phe Tyr Cys Glu Gly Phe Arg Pro Asn Lys Pro Tyr Lys Pro Lys Met Trp Thr Glu Val Trp Thr	253
823	GGC TGG TAT ACG AAA TTC GGT GGT CCA ATT CCT CAA AGA CCA GCC GAA GAC ATT GCA TTT TCA GTT GCC	891
254	Gly Trp Tyr Thr Lys Phe Gly Gly Pro Ile Pro Gln Arg Pro Ala Glu Asp Ile Ala Phe Ser Val Ala	276
892	AGG TTT GTT CAG AAC AAT GGT TCA TTC TTC AAT TAC TAC ATG TAT CAT GGA GGA ACA AAT TTT GGC CGG	960
277	Arg Phe Val Gln Asn Asn Gly Ser Phe Phe Asn Tyr Tyr Met Tyr His Gly Gly Thr Asn Phe Gly Arg	299
961	ACA TCA TCA GGG CTT TTC ATT GCA ACT AGC TAC GAT TAT GAT GCT CCT CTC GAT GAA TAT GGG TTG CTG	1029
300	Thr Ser Ser Gly Leu Phe Ile Ala Thr Ser Tyr Asp Tyr Asp Ala Pro Leu Asp Glu Tyr Gly Leu Leu	322
1030	AAT GAA CCA AAG TAT GGG CAC TTG AGA GAC TTA CAT AAA GCT ATC AAG CTA TCT GAA CCG GCT TTA GTT	1098
323	Asn Glu Pro Lys Tyr Gly His Leu Arg Asp Leu His Lys Ala Ile Lys Leu Ser Glu Pro Ala Leu Val	345
1099	TCA TCA TAT GCT GCG GTG ACT AGT CTT GGA AGT AAT CAA GAG GCT CAT GTT TAT AGA TCA AAA TCT GGA	1167
346	Ser Ser Tyr Ala Ala Val Thr Ser Leu Gly Ser Asn Gln Glu Ala His Val Tyr Arg Ser Lys Ser Gly	368
1168	GCT TGT GCT GCT TTT TTA TCC AAC TAT GAC TCT AGA TAT TCA GTA AAA GTC ACC TTT CAG AAT AGG CCA	1236
369	Ala Cys Ala Ala Phe Leu Ser Asn Tyr Asp Ser Arg Tyr Ser Val Lys Val Thr Phe Gln Asn Arg Pro	391
1237	TAC AAT CTG CCT CCA TGG TCC ATC AGC ATT CTT CCC GAC TGC AAA ACT GCC GTT TAC AAC ACT GCA CAG	1305
392	Tyr Asn Leu Pro Pro Trp Ser Ile Ser Ile Leu Pro Asp Cys Lys Thr Ala Val Tyr Asn Thr Ala Gln	414
1306	GTT AAC TCT CAA AGC TCG AGC ATA AAG ATG ACG CCT GCA GGT GGT GGA TTG TCT TGG CAG TCA TAC AAT	1374
415	Val Asn Ser Gln Ser Ser Ser Ile Lys Met Thr Pro Ala Gly Gly Gly Leu Ser Trp Gln Ser Tyr Asn	437
1375	GAA GAA ACG CCT ACT GCT GAT GAC AGC GAT ACA CTT ACA GCT AAC GGA CTA TGG GAA CAG AAA AAC GTC	1443
438	Glu Glu Thr Pro Thr Ala Asp Asp Ser Asp Thr Leu Thr Ala Asn Gly Leu Trp Glu Gln Lys Asn Val	460

Figure 2
Sheet 8 of 12Gene/clone name: TBG4/pZBG2-/pTomβgal4; accession number AF0203 Sequence ID number 4
cont.

1444	ACA AGA GAT TCA TCA GAC TAT CTG TGG TAC ATG ACA AAT GTA AAT ATA GCA TCT AAT GAA GGA TTT CTA	1512
461	Thr Arg Asp Ser Ser Asp Tyr Leu Trp Tyr Met Thr Asn Val Asn Ile Ala Ser Asn Glu Gly Phe Leu	483
1513	AAG AAC GGA AAG GAT CCT TAT CTC ACT GTT ATG TCC GCT GGT CAT GTC TTG CAT GTT TTC GTC AAT GGA	1581
484	Lys Asn Gly Lys Asp Pro Tyr Leu Thr Val Met Ser Ala Gly His Val Leu His Val Phe Val Asn Gly	506
1582	AAA CTA TCA GGA ACT GTT TAT GGT ACA TTG GAT AAT CCA AAA CTT ACA TAC AGT GGC AAC GTG AAG TTA	1650
507	Lys Leu Ser Gly Thr Val Tyr Gly Thr Leu Asp Asn Pro Lys Leu Thr Tyr Ser Gly Asn Val Lys Leu	529
1651	AGA GCT GGT ATT AAC AAG ATT TCT CTG CTC AGT GTT TCC GTT GGT CTC CCG AAC GTT GGC GTG CAT TAT	1719
530	Arg Ala Gly Ile Asn Lys Ile Ser Leu Leu Ser Val Ser Val Gly Leu Pro Asn Val Gly Val His Tyr	552
1720	GAT ACA TGG AAT GCA GGA GTT CTA GGT CCA GTC ACG TTG AGC GGT CTC AAT GAA GGG TCA AGA AAC TTG	1788
553	Asp Thr Trp Asn Ala Gly Val Leu Gly Pro Val Thr Leu Ser Gly Leu Asn Glu Gly Ser Arg Asn Leu	575
1789	GCG AAA CAG AAA TGG TCT TAC AAG GTT GGT CTG AAA GGC GAA TCG TTA AGT CTT CAC TCC TTA AGT GCG	1857
576	Ala Lys Gln Lys Trp Ser Tyr Lys Val Gly Leu Lys Gly Glu Ser Leu Ser Leu His Ser Leu Ser Gly	598
1858	AGT TCT TCT GTT GAA TGG GTT CGA GGT TCA CTA ATG GCT CAA AAG CAG CCC CTG ACT TGG TAC AAG GCT	1926
599	Ser Ser Ser Val Glu Trp Val Arg Gly Ser Leu Met Ala Gln Lys Gln Pro Leu Thr Trp Tyr Lys Ala	621
1927	ACA TTT AAC GCG CCT GGA GGA AAT GAT CCA CTA GCT TTA GAC ATG GCA AGT ATG GGA AAA GGT CAG ATA	1995
622	Thr Phe Asn Ala Pro Gly Gly Asn Asp Pro Leu Ala Leu Asp Met Ala Ser Met Gly Lys Gly Gln Ile	644
1996	TGG ATA AAT GGT GAA GGC GTA GGT CGC CAT TGG CCT GGA TAC ATA GCA CAA GGC GAC TGC AGC AAA TGC	2064
645	Trp Ile Asn Gly Glu Gly Val Gly Arg His Trp Pro Gly Tyr Ile Ala Gln Gly Asp Cys Ser Lys Cys	667
2065	AGT TAT GCT GGA ACG TTC AAC GAG AAG AAG TGC CAG ACT AAC TGC GGA CAA CCT TCT CAG AGA TGG TAC	2133
668	Ser Tyr Ala Gly Thr Phe Asn Glu Lys Lys Cys Gln Thr Asn Cys Gly Gln Pro Ser Gln Arg Trp Tyr	690
2134	CAT GTT CCA CGA TCG TGG CTG AAA CCA AGT GGA AAC TTG TTA GTA GTA TTC GAA GAA TGG GGA GGT AAT	2202
691	His Val Pro Arg Ser Trp Leu Lys Pro Ser Gly Asn Leu Leu Val Val Phe Glu Glu Trp Gly Gly Asn	713
2203	CCA ACA GGA ATT TCT CTA GTC AGG AGA TCA AGA TAA AGA AACTCGAAAAAGTAAACCTTGTTTCAGTAAGTATGGTGTGAA	2282
714	Pro Thr Gly Ile Ser Leu Val Arg Arg Ser Arg ***	725
2283	TTGCGCGCCGAAAAATACATACACGAAGCTAACAATGGAGGCTACAGTTTGCAAAATTCAGCTGAATAAAACATTAGAAGATAAAGAAATATT	2374
2375	TGATTAAAAGGAGTATATAAATTTACAGAGAATTTTCTTTATTTCTTTGTAAACCTTTGGTTTATAAAGTTTATACAGAAATTTTCGTGTTATT	2466
2467	GGATTATGAGATTGAAGAAGATTGTACAGCTTCCAAATACTATTAGAATACAAATAAATTTTCATGTAAAAA	2554

Figure 2
Sh 19 of 12

Gene/clone name: TBG5/RT-PCR2-1/b1; accession number AF154423; sequence ID number 5

1 ATC CAG ACT TAC GTT TTC TGG AAC CTT CAT GAA CCT GTT CGA AAT CAG TAT GAT TTT GAA GGA AGG AAA	69
1 Ile Gln Thr Tyr Val Phe Trp Asn Leu His Glu Pro Val Arg Asn Gln Tyr Asp Phe Glu Gly Arg Lys	23
70 GAT TTG ATT AAT TTT GTG AAG TTG GTG GAG AGA GCT GGC TTA TTT GTT CAT ATA AGG ATT GGG CCT TAT	138
24 Asp Leu Ile Asn Phe Val Lys Leu Val Glu Arg Ala Gly Leu Phe Val His Ile Arg Ile Gly Pro Tyr	46
139 GTT TGT GCA GAA TGG AAC TAT GGT GGG TTT CCT CTT TGG TTG CAT TTC ATT CCT GGA ATT GAA TTT CGA	207
47 Val Cys Ala Glu Trp Asn Tyr Gly Gly Phe Pro Leu Trp Leu His Phe Ile Pro Gly Ile Glu Phe Arg	69
208 ACC GAC AAT GAA CCG TTC AAG GCA GAA ATG AAG CGA TTC ACA GCT AAA ATT GTT GAC ATG ATC AAG CAA	276
70 Thr Asp Asn Glu Pro Phe Lys Ala Glu Met Lys Arg Phe Thr Ala Lys Ile Val Asp Met Ile Lys Gln	92
277 GAA AAT CTA TAT GCA TCC CAG GGT GGG CCG GTT ATC TTG TCT CAG ATA GAA AAT GAG TAT GGC AAT GGT	345
93 Glu Asn Leu Tyr Ala Ser Gln Gly Gly Pro Val Ile Leu Ser Gln Ile Glu Asn Glu Tyr Gly Asn Gly	115
346 GAT ATT GAG TCT CGT TAT GGT CCT CGT GCC AAA CCT TAC GTG AAC TGG GCA GCA TCA ATG GCT ACG TCT	414
116 Asp Ile Glu Ser Arg Tyr Gly Pro Arg Ala Lys Pro Tyr Val Asn Trp Ala Ala Ser Met Ala Thr Ser	138
415 TTA AAT ACG GGA GTG CCA TGG GTT ATG TGT CAG CAA CCA GAT GCC CCT CCT TCC GTT ATT AAC ACT TGC	483
139 Leu Asn Thr Gly Val Pro Trp Val Met Cys Gln Gln Pro Asp Ala Pro Pro Ser Val Ile Asn Thr Cys	161
484 AAT GGA TTT TAT TGT GAC CAA TTC AAG CAA AAT TCC GAT AAA ACA CCC AAG ATG TGG ACT GAG AAT TGG	552
162 Asn Gly Phe Tyr Cys Asp Gln Phe Lys Gln Asn Ser Asp Lys Thr Pro Lys Met Trp Thr Glu Asn Trp	184
553 ACC GGA TGG TTT CTG TGG TTT GGT GGT CCT GTC CCT TAC AGA CCA GTG GAA GAC ATC GCT TTC GCT GTG	621
185 Thr Gly Trp Phe Leu Ser Phe Gly Gly Pro Val Pro Tyr Arg Pro Val Glu Asp Ile Ala Phe Ala Val	207
622 GCT CGA TTT TTC CAG CGA GGC GGA ACT TTC CAG AAC TAT TAC ATG TAC CAC GGG GGA ACT AAC TTT GGG	690
208 Ala Arg Phe Phe Gln Arg Gly Gly Thr Phe Gln Asn Tyr Tyr Met Tyr His Gly Gly Thr Asn Phe Gly	230
691 AGA ACC AGT GGT GGA CCG TTT ATT GCA ACT AGC TAT GAC TAT GAT GCC CCT CTC GAC GAA TAC GG	755
231 Arg Thr Ser Gly Gly Pro Phe Ile Ala Thr Ser Tyr Asp Tyr Asp Ala Pro Leu Asp Glu Tyr	252

11/31

Figure 2
Sheet 10 of 12

Gene/clone name: TBG6/RT-2-6/b1; accession number AF154424; Sequence ID number 5

1	ATC CAG ACA TAT GTT TTT TGG AAT GTT CAT GAG CCT TCT CCT GGC AAT TAC AAT TTT GAA GGA AGA TAT	69
1	Ile Gln Thr Tyr Val Phe Trp Asn Val His Glu Pro Ser Pro Gly Asn Tyr Asn Phe Glu Gly Arg Tyr	23
70	GAC CTG GTG AGG TTT GTA AAA ACG ATT CAG AAA GCA GGG CTG TAT GCT CAT CTT CGA ATT GGC CCT TAC	138
24	Asp Leu Val Arg Phe Val Lys Thr Ile Gln Lys Ala Gly Leu Tyr Ala His Leu Arg Ile Gly Pro Tyr	46
139	GTT TGT GCA GAG TGG AAT TTT GGA GGG TTT CCA GTA TGG CTG AAG TAT GTA CCT GGC ATT AGC TTC AGA	207
47	Val Cys Ala Glu Trp Asn Phe Gly Gly Phe Pro Val Trp Leu Lys Tyr Val Pro Gly Ile Ser Phe Arg	69
208	GCT GAT AAT GAA CCT TTC AAG AAC GCA ATG AAA GGG TAT GCT GAG AAA ATT GTT AAC TTG ATG AAG ATC	276
70	Ala Asp Asn Glu Pro Phe Lys Asn Ala Met Lys Gly Tyr Ala Glu Lys Ile Val Asn Leu Met Lys Ile	92
277	ATA ATC TTT TCG AGT CTC ACG GTG GTC CAA TCA TAC TCT CAC AGA TTG AGA ATG AGT ATG GGC CTC AAG	345
93	Ile Ile Phe Ser Ser Leu Arg Val Val Gln Ser Tyr Ser His Arg Leu Arg Met Ser Met Gly Leu Lys	115
346	CCA AGG TAC TTG GAG CAC CGG GAC ATC AGT ATT CAA CAT GGG CTG CAA ATA TGG CAG TTG GAT TTG AAC	414
116	Pro Arg Tyr Leu Glu His Arg Asp Ile Ser Ile Gln His Gly Leu Gln Ile Trp Gln Leu Asp Leu Asn	138
415	ACA GGC GTC CCA TGG GTG ATG TGC AAG GAA GAA GAT GCA CCA GAT CCT GTG ATC AAC ACA TGC AAT GGT	483
139	Thr Gly Val Pro Trp Val Met Cys Lys Glu Glu Asp Ala Pro Asp Pro Val Ile Asn Thr Cys Asn Gly	161
484	TTC TAC TGT GAT AAT TTC TTC CCA AAC AAA CCA TAC AAA CCT GCA ATT TGG ACT GAA GCT TGG AGT GGA	552
162	Phe Tyr Cys Asp Asn Phe Phe Pro Asn Lys Pro Tyr Lys Pro Ala Ile Trp Thr Glu Ala Trp Ser Gly	184
553	TGG TTC TCG GAA TTT GGC GGT CCC CTT CAT CAG AGA CCA GTT CAG GAT TTG GCA TTT GCT GTT GCC CAA	621
185	Trp Phe Ser Glu Phe Gly Gly Pro Leu His Gln Arg Pro Val Gln Asp Leu Ala Phe Ala Val Ala Gln	207
622	TTT ATA CAA AGA GGA GGA TCT TTT GTT AAC TAT TAC ATG TAC CAT GGG GGC ACG AAC TTT GGA CGC ACT	690
208	Phe Ile Gln Arg Gly Gly Ser Phe Val Asn Tyr Tyr Met Tyr His Gly Gly Thr Asn Phe Gly Arg Thr	230
691	GCG GGT GGG CCA TTC ATC ACT ACC AGC TAT GAT TAT GAT CCC CCC CTC GAC GAG TAT GG	749
231	Ala Gly Gly Pro Phe Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Leu Asp Glu Tyr	250

1	GCMACTTCTCCT																												12	
13	GTGAATAACACCGGTAACGGCCAATGCCAACTCTCGTCGGAATCTGAATAGTGATTTAAGCAGCTTAGCTAGCTAACTTTTGCCCTCTGCA																												103	
104	ATG	AAC	ACA	ATG	AGT	TGT	TTG	TCC	TCT	AAT	TTC	AAG	TTC	GTT	TTC	CTT	GCC	TCG	ACT	GTG	ATA	TGG	ATG							172
1	Met	Asn	Thr	Met	Ser	Cys	Leu	Ser	Ser	Asn	Phe	Lys	Phe	Val	Phe	Leu	Ala	Ser	Thr	Val	Ile	Trp	Met							23
173	ACG	GTA	ATG	TCG	TCG	TCG	TTA	GCA	GCA	GTA	GAT	GCT	TCC	AAT	GTT	ACT	ACT	ATT	GGT	ACT	GAT	AGT	GTG							241
24	Thr	Val	Met	Ser	Ser	Ser	Leu	Ala	Ala	Val	Asp	Ala	Ser	Asn	Val	Thr	Thr	Ile	Gly	Thr	Asp	Ser	Val							46
242	ACT	TAC	GAT	CGA	CGC	TCG	TTG	ATT	ATT	AAC	GGC	CAG	AGG	AAG	CTG	CTC	ATC	TCC	GCT	TCC	ATT	CAC	TAT							310
47	Thr	Tyr	Asp	Arg	Arg	Ser	Leu	Ile	Ile	Asn	Gly	Gln	Arg	Lys	Leu	Leu	Ile	Ser	Ala	Ser	Ile	His	Tyr							69
311	CCT	CGC	AGT	GTC	CCT	GCC	ATG	TGG	CCT	GGT	CTG	GTT	CGA	TTG	GCG	AAG	GAA	GGA	GGA	GTG	GAT	GTT	ATT							379
70	Pro	Arg	Ser	Val	Pro	Ala	Met	Trp	Pro	Gly	Leu	Val	Arg	Leu	Ala	Lys	Glu	Gly	Gly	Val	Asp	Val	Ile							92
380	GAA	ACG	TAT	GTT	TTC	TGG	AAC	GGT	CAC	GAA	CCT	TCT	CCG	GGC	AAT	TAT	TAC	TTT	GGA	GGA	AGG	TTT	GAT							448
93	Glu	Thr	Tyr	Val	Phe	Trp	Asn	Gly	His	Glu	Pro	Ser	Pro	Gly	Asn	Tyr	Tyr	Phe	Gly	Gly	Arg	Phe	Asp							115
449	CTA	GTC	AAA	TTT	TGT	AAG	ATC	ATT	CAG	CAG	GCT	GGA	ATG	TAT	ATG	ATT	CTT	CGG	ATT	GGA	CCA	TTT	GTA							517
116	Leu	Val	Lys	Phe	Cys	Lys	Ile	Ile	Gln	Gln	Ala	Gly	Met	Tyr	Met	Ile	Leu	Arg	Ile	Gly	Pro	Phe	Val							138
518	GCT	GCA	GAA	TGG	AAC	TTT	GGT	GGA	CTT	CCT	GTG	TGG	TTG	CAT	TAT	GTG	CCA	GGT	ACC	ACC	TTT	CGG	ACT							586
139	Ala	Ala	Glu	Trp	Asn	Phe	Gly	Gly	Leu	Pro	Val	Trp	Leu	His	Tyr	Val	Pro	Gly	Thr	Thr	Phe	Arg	Thr							161
587	GAT	AGT	GAA	CCA	TTT	AAG	TAT	CAC	ATG	CAG	AAG	TTC	ATG	ACA	TAT	ACA	GTG	AAC	TTA	ATG	AAG	AGA	GAG							655
162	Asp	Ser	Glu	Pro	Phe	Lys	Tyr	His	Met	Gln	Lys	Phe	Met	Thr	Tyr	Thr	Val	Asn	Leu	Met	Lys	Arg	Glu							184
656	AGG	CTT	TTT	GCA	TCT	CAA	GGA	GGT	CCA	ATC	ATC	TTG	TCA	CAG	GTA	GAA	AAT	GAG	TAC	GGC	TAC	TAT	GAA							724
185	Arg	Leu	Phe	Ala	Ser	Gln	Gly	Gly	Pro	Ile	Ile	Leu	Ser	Gln	Val	Glu	Asn	Glu	Tyr	Gly	Tyr	Tyr	Glu							207
725	AAT	GCA	TAT	GGA	GAA	GGA	GGG	AAA	AGG	TAT	GCC	TTA	TGG	GCT	GCT	AAA	ATG	GCC	CTT	TCT	CAA	AAT	ACT							793
208	Asn	Ala	Tyr	Gly	Glu	Gly	Gly	Lys	Arg	Tyr	Ala	Leu	Trp	Ala	Ala	Lys	Met	Ala	Leu	Ser	Gln	Asn	Thr							230
794	GGT	GTA	CCT	TGG	ATA	ATG	TGC	CAG	CAG	TAT	GAT	GCT	CCT	GAT	CCT	GTG	ATT	GAC	ACA	TGC	AAT	TCA	TTT							862
231	Gly	Val	Pro	Trp	Ile	Met	Cys	Gln	Gln	Tyr	Asp	Ala	Pro	Asp	Pro	Val	Ile	Asp	Thr	Cys	Asn	Ser	Phe							253
863	TAC	TGC	GAC	CAA	TTT	AAA	CCA	ATC	TCT	CCA	AAC	AAG	CCC	AAA	ATT	TGG	ACA	GAG	AAC	TGG	CCG	GGA	TGG							931
254	Tyr	Cys	Asp	Gln	Phe	Lys	Pro	Ile	Ser	Pro	Asn	Lys	Pro	Lys	Ile	Trp	Thr	Glu	Asn	Trp	Pro	Gly	Trp							276
932	TTC	AAG	ACA	TTT	GGG	GCC	AGA	GAT	CCT	CAC	AGG	CCT	GCA	GAA	GAT	GTT	GCT	TAT	TCC	GTG	GCT	CGT	TTT							1000
277	Phe	Lys	Thr	Phe	Gly	Ala	Arg	Asp	Pro	His	Arg	Pro	Ala	Glu	Asp	Val	Ala	Tyr	Ser	Val	Ala	Arg	Phe							299
1001	TTC	CAA	AAA	GGA	GGA	AGC	GTG	CAG	AAT	TAT	TAC	ATG	TAC	CAT	GGT	GGG	ACG	AAC	TTT	GGC	AGG	ACA	GCA							1069
300	Phe	Gln	Lys	Gly	Gly	Ser	Val	Gln	Asn	Tyr	Tyr	Met	Tyr	His	Gly	Gly	Thr	Asn	Phe	Gly	Arg	Thr	Ala							322
1070	GGT	GGC	CCT	TTC	ATT	ACC	ACA	AGT	TAT	GAC	TAT	GAT	GCC	CCA	ATT	GAC	GAA	TAT	GGT	TTA	CCA	AGG	TTT							1138
323	Gly	Gly	Pro	Phe	Ile	Thr	Thr	Ser	Tyr	Asp	Tyr	Asp	Ala	Pro	Ile	Asp	Glu	Tyr	Gly	Leu	Pro	Arg	Phe							345
1139	CCA	AAA	TGG	GGT	CAC	CTT	AAA	GAA	CTT	CAT	AAA	GTC	ATA	AAA	TCG	TGT	GAG	CAT	GCT	CTG	CTG	AAC	AAT							1207
346	Pro	Lys	Trp	Gly	His	Leu	Lys	Glu	Leu	His	Lys	Val	Ile	Lys	Ser	Cys	Glu	His	Ala	Leu	Leu	Asn	Asn							368
1208	GAT	CCA	ACT	CTT	CTT	TCA	TTA	GGT	CCT	CTA	CAA	GAG	GCT	GAT	GTT	TAT	GAA	GAT	GCT	TCA	GGC	GCT	TGT							1276
369	Asp	Pro	Thr	Leu	Leu	Ser	Leu	Gly	Pro	Leu	Gln	Glu	Ala	Asp	Val	Tyr	Glu	Asp	Ala	Ser	Gly	Ala	Cys							391
1277	GCT	GCC	TTT	CTC	GCG	AAT	ATG	GAT	GAC	AAA	AAT	GAC	AAG	GTG	GTA	CAG	TTC	CGA	CAT	GTA	TCA	TAC	CAC							1345
392	Ala	Ala	Phe	Leu	Ala	Asn	Met	Asp	Asp	Lys	Asn	Asp	Lys	Val	Val	Gln	Phe	Arg	His	Val	Ser	Tyr	His							414
1346	TTG	CCA	GCA	TGG	TCT	GTT	AGC	ATT	TTG	CCA	GAC	TGC	AAA	AAT	GTA	GCG	TTC	AAC	ACA	GCA	AAG	GTT	GGA							1414
415	Leu	Pro	Ala	Trp	Ser	Val	Ser	Ile	Leu	Pro	Asp	Cys	Lys	Asn	Val	Ala	Phe	Asn	Thr	Ala	Lys	Val	Gly							437
1415	TGT	CAA	ACT	TCT	ATT	GTC	AAT	ATG	GCA	CCC	ATA	GAT	TTG	CAT	CCC	ACC	GCA	AGT	TCA	CCA	AAG	AGA	GAC							1483
438	Cys	Gln	Thr	Ser	Ile	Val	Asn	Met	Ala	Pro	Ile	Asp	Leu	His	Pro	Thr	Ala	Ser	Ser	Pro	Lys	Arg	Asp							460

Figur 2
Sheet 12 of 12

Gene/clone name: TBG7/pZBG-18; accession number AF154422; Sequence ID number 7 cont.

1484	ATC	AAG	TCT	CTT	CAG	TGG	GAA	GTC	TTC	AAG	GAA	ACA	GCT	GGA	GTA	TGG	GGA	GTT	GCT	GAT	TTC	ACT	AAA	1552
461	Ile	Lys	Ser	Leu	Gln	Trp	Glu	Val	Phe	Lys	Glu	Thr	Ala	Gly	Val	Trp	Gly	Val	Ala	Asp	Phe	Thr	Lys	483
1553	AAC	GGA	TTT	GTA	GAT	CAC	ATT	AAC	ACC	ACA	AAA	GAT	GCT	ACA	GAC	TAC	CTC	TGG	TAC	ACA	ACA	AGT	ATT	1621
484	Asn	Gly	Phe	Val	Asp	His	Ile	Asn	Thr	Thr	Lys	Asp	Ala	Thr	Asp	Tyr	Leu	Trp	Tyr	Thr	Thr	Ser	Ile	506
1622	TTT	GTT	CAT	GCA	GAG	GAG	GAT	TTC	CTA	AGA	AAC	AGA	GGC	ACT	GCA	ATG	CTT	TTC	GTT	GAA	TCA	AAG	GGT	1690
507	Phe	Val	His	Ala	Glu	Glu	Asp	Phe	Leu	Arg	Asn	Arg	Gly	Thr	Ala	Met	Leu	Phe	Val	Glu	Ser	Lys	Gly	529
1691	CAT	GCT	ATG	CAT	GTC	TTC	ATC	AAT	AAA	AAG	CTT	CAA	GCC	AGT	GCA	TCT	GGA	AAT	GGC	ACA	GTG	CCA	CAG	1759
530	His	Ala	Met	His	Val	Phe	Ile	Asn	Lys	Lys	Leu	Gln	Ala	Ser	Ala	Ser	Gly	Asn	Gly	Thr	Val	Pro	Gln	552
1760	TTC	AAG	TTT	GGA	ACT	CCT	ATT	GCT	CTA	AAG	GCA	GGG	AAG	AAT	GAA	ATT	TCC	TTG	TTA	AGC	ATG	ACT	GTG	1828
553	Phe	Lys	Phe	Gly	Thr	Pro	Ile	Ala	Leu	Lys	Ala	Gly	Lys	Asn	Glu	Ile	Ser	Leu	Leu	Ser	Met	Thr	Val	575
1829	GGC	CTA	CAA	ACA	GCT	GGA	GCG	TTT	TAT	GAA	TGG	ATT	GGA	GCT	GGT	CCA	ACA	AGT	GTC	AAA	GTT	GCA	GGG	1897
576	Gly	Leu	Gln	Thr	Ala	Gly	Ala	Phe	Tyr	Glu	Trp	Ile	Gly	Ala	Gly	Pro	Thr	Ser	Val	Lys	Val	Ala	Gly	598
1898	TTC	AAG	ACT	GGG	ACT	ATG	GAC	TTG	ACT	GCG	TCT	GCT	TGG	ACC	TAT	AAG	ATT	GGA	TTG	CAA	GGA	GAA	CAT	1966
599	Phe	Lys	Thr	Gly	Thr	Met	Asp	Leu	Thr	Ala	Ser	Ala	Trp	Thr	Tyr	Lys	Ile	Gly	Leu	Gln	Gly	Glu	His	621
1967	TTG	AGG	ATA	CAG	AAG	TCA	TAT	AAC	TTG	AAG	AGT	AAA	ATT	TGG	GCA	CCA	ACT	TCG	CAG	CCA	CCA	AAG	CAA	2035
622	Leu	Arg	Ile	Gln	Lys	Ser	Tyr	Asn	Leu	Lys	Ser	Lys	Ile	Trp	Ala	Pro	Thr	Ser	Gln	Pro	Pro	Lys	Gln	644
2036	CAG	CCC	CTC	ACA	TGG	TAT	AAG	GCA	GTA	GTA	GAT	GCG	CCT	CCT	GGT	AAT	GAA	CCT	GTT	GCA	CTT	GAT	ATG	2104
645	Gln	Pro	Leu	Thr	Trp	Tyr	Lys	Ala	Val	Val	Asp	Ala	Pro	Pro	Gly	Asn	Glu	Pro	Val	Ala	Leu	Asp	Met	667
2105	ATT	CAT	ATG	GGA	AAA	GGA	ATG	GCT	TGG	TTG	AAT	GGA	CAA	GAA	ATT	GGC	AGA	TAT	TGG	CCG	AGG	AGA	ACT	2173
668	Ile	His	Met	Gly	Lys	Gly	Met	Ala	Trp	Leu	Asn	Gly	Gln	Glu	Ile	Gly	Arg	Tyr	Trp	Pro	Arg	Arg	Thr	690
2174	TCT	AAA	TAT	GAG	AAT	TGT	GTT	ACT	CAA	TGT	GAC	TAC	AGA	GGC	AAA	TTT	AAC	CCT	GAT	AAG	TGT	GTC	ACT	2242
691	Ser	Lys	Tyr	Glu	Asn	Cys	Val	Thr	Gln	Cys	Asp	Tyr	Arg	Gly	Lys	Phe	Asn	Pro	Asp	Lys	Cys	Val	Thr	713
2243	GGC	TGT	GGA	CAA	CCT	ACA	CAG	AGA	TGG	TAT	CAT	GTG	CCA	CGA	TCT	TGG	TTC	AAG	CCA	TCA	GGA	AAT	GTC	2311
714	Gly	Cys	Gly	Gln	Pro	Thr	Gln	Arg	Trp	Tyr	His	Val	Pro	Arg	Ser	Trp	Phe	Lys	Pro	Ser	Gly	Asn	Val	736
2312	TTA	ATT	ATC	TTT	GAG	GAA	ATA	GGT	GGA	GAT	CCC	TCT	CAA	ATT</										

DNASIS
Multiple Edit1Figure 3
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	10	20	30	40	50	
TBG1-ORF	-24MGFWMA	MLMLLLCLW	VSCGISVSYD	26
TBG2-ORF	-14MSRRKT	LNFPILITVL	TIHFVIVAGE	36
TBG3-ORF	-20	MGCTLLMLN	VLLVLLGSWV	30
TBG4-ORF	-22MLRTNVLL	LLVTCILDFE	28
TBG5-ORF	1	-----	-----	-----	-----	50
TBG6-ORF	1	-----	-----	-----	-----	50
TBG7-ORF	-1	..MNTMSCLSS	NFKFVFLAST	VIWMIVMSSS	LAAVDASNT	49
apple	-21MGVGIOIMW	SILLFSCIF	29
carnation	-16MLCG	KENNVMMML	34
asparagus	-20MALKLVLML	VALLAAVWSP	30
broccoli	-20MKMKOFNLLS	LFLLITTSFG	30
Lupin	-12MEGSRIVM	ESLMSRRNFH	MVLLALFFWV	38
	60	70	80	90	100	
TBG1-ORF	27	HKALIVNGOR	KLLTSSSTHY	RRSTPEMWP	LLOKAKEGGV	76
TBG2-ORF	37	NRALFEGGKR	RMHSAGHTY	BRATPEMWT	LRARSKEGGA	86
TBG3-ORF	31	HRALIVNGOR	KLLTSSSVHY	RRSTPEMWP	ILLOKAKEGGV	80
TBG4-ORF	29	DRALFEGGKR	KLLTSSSTHY	RRSTPEMWP	LLOKAKEGGV	78
TBG5-ORF	51	-----	-----	-----	-----	100
TBG6-ORF	51	-----	-----	-----	-----	100
TBG7-ORF	50	RRSLFEGGKR	KLLTSSSTHY	RRSTPEMWP	ILLOKAKEGGV	99
apple	30	HKALFEGGKR	KLLTSSSTHY	RRSTPEMWP	ILLOKAKEGGV	79
carnation	35	YRAKINDOR	KLLTSSSTHY	RRSTPEMWP	ILLOKAKEGGV	84
asparagus	31	HKSIVNGOR	KLLTSSSTHY	RRSTPEMWP	ILLOKAKEGGV	80
broccoli	31	ERKALIDGOR	KLLTSSSTHY	RRSTPEMWP	ILLOKAKEGGV	80
Lupin	39	HKALFEGGKR	KLLTSSSTHY	RRSTPEMWP	ILLOKAKEGGV	88
	110	120	130	140	150	
TBG1-ORF	77	GHEPSEGKYV	FEERYDHY	RVVGEAGYV	VHLRIGGAG	126
TBG2-ORF	87	GHEPSEGKYV	FEERYDHY	RVVGEAGYV	VHLRIGGAG	136
TBG3-ORF	81	GHEPSEGKYV	FEERYDHY	RVVGEAGYV	VHLRIGGAG	130
TBG4-ORF	79	GHEPSEGKYV	FEERYDHY	RVVGEAGYV	VHLRIGGAG	128
TBG5-ORF	101	LHSGVRNOYD	FEERYDHY	RVVGEAGYV	VHLRIGGAG	150
TBG6-ORF	101	VHESGNYN	FEERYDHY	RVVGEAGYV	VHLRIGGAG	150
TBG7-ORF	100	GHEPSEGKYV	FEERYDHY	RVVGEAGYV	VHLRIGGAG	149
apple	80	GHEPSEGKYV	FEERYDHY	RVVGEAGYV	VHLRIGGAG	129
carnation	85	GHEPSEGKYV	FEERYDHY	RVVGEAGYV	VHLRIGGAG	134
asparagus	81	GHEPSEGKYV	FEERYDHY	RVVGEAGYV	VHLRIGGAG	130
broccoli	81	AHEPSEGKYV	FEERYDHY	RVVGEAGYV	VHLRIGGAG	130
Lupin	89	GHEPSEGKYV	FEERYDHY	RVVGEAGYV	VHLRIGGAG	138
	160	170	180	190	200	
TBG1-ORF	127	WLKVPGISF	RTDNEPFKAA	MOKETKIVD	MMK-----AE	176
TBG2-ORF	137	WLKVPGLIF	RTDNEPFKAA	MOKETKIVD	MMK-----AE	186
TBG3-ORF	131	WLKVPGISF	RTDNEPFKAA	MOKETKIVD	MMK-----AE	180
TBG4-ORF	129	WLKVPGMEF	RTDNEPFKAA	MOKETKIVD	MMK-----AE	178
TBG5-ORF	151	WLHFIPIGIEF	RTDNEPFKAA	MOKETKIVD	MMK-----AE	200
TBG6-ORF	151	WLKVPGISF	RTDNEPFKAA	MOKETKIVD	MMK-----AE	200
TBG7-ORF	150	WLHVPGLTF	RTDNEPFKAA	MOKETKIVD	MMK-----AE	199
apple	130	WLKVPGIAF	RTDNEPFKAA	MOKETKIVD	MMK-----AE	179
carnation	135	WLKVPGIEF	RTDNEPFKAA	MOKETKIVD	MMK-----AE	184
asparagus	131	WLKVPGIHF	RTDNEPFKAA	MOKETKIVD	MMK-----AE	180
broccoli	131	WLHNPDMKF	RTDNEPFKAA	MOKETKIVD	MMK-----AE	180
Lupin	139	WLKVPGIAF	RTDNEPFKAA	MOKETKIVD	MMK-----AE	188
	210	220	230	240	250	
TBG1-ORF	177	ILSQ-IENEY	GP--MEWELG	EPGKVYSEWA	AKMAVDLGTG	226
TBG2-ORF	187	ILLQ-IENEY	GN--VESSFG	PKGKLYMKWA	AEMAVGLGAG	236
TBG3-ORF	181	ILSQ-IENEY	GP--MEWELG	APGKSYAQA	AKMAVGLDTG	230
TBG4-ORF	179	IMAQ-IENEY	GP--MEWELG	APGKAYTKWA	AQMAVGLKTG	228
TBG5-ORF	201	ILSQ-IENEY	GNGDIESRYG	PRAKPYVNW	ASMATSLNTG	250
TBG6-ORF	201	RMSMGLKPRY	----LEHRDI	SIQHGLQIWQ	----LDLNTG	250
TBG7-ORF	200	ILSQ-VENEY	G--YYENAYG	EGGKRYALWA	AKMALSONTG	249
apple	180	ILSQ-IENEF	GP--VEWEIG	APGKAYTKWA	AQMAVGLDTG	229
carnation	185	ILNQ-IENEY	GP--VEWEIG	APGKAYTHWA	AQMAQSLNAG	234

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Sh et 2 f 4

asparagus	181	ATCG--TENEY	GP--VEYVDG	AAGKSYINWA	ACGAYGHWG	GVAVMKOB-	230
broccoli	181	ATCG--TENEY	GN--VISSYG	AEGKAYIDAC	ANWANSBDE	GVAVMKOB-	230
Lupin	189	ATCG--TENEY	GP--VEWEIG	APGKAYTWA	ACGAYGHWG	GVAVMKOB-	238
		260	270	280	290	300	
TBG1-ORF	227	DVDPDIINTC	NGFYCDYFTP	NKANKPKMT	EAWTAWTIC	GVAVMKOB-	276
TBG2-ORF	237	DAPEYIINTC	NAYYCDGFTP	NSEKKPKMT	ENWNGWADW	GERLPYRPE	286
TBG3-ORF	231	DAPDPIINAC	NGFYCDYFSP	NKAYKPKMT	EAWTAWTIC	GVAVMKOB-	280
TBG4-ORF	229	DAPDPVIDTC	NGFYCDGFRP	NKRYKPKMT	ENWNGWADW	GERLPYRPE	278
TBG5-ORF	251	DAPPSVINTC	NGFYCDQPKQ	NSDKTPKMT	ENWNGWADW	GERLPYRPE	300
TBG6-ORF	251	DAPDPVINTC	NGFYCDNFFP	NKPKPKMT	ENWNGWADW	GERLPYRPE	300
TBG7-ORF	250	DAPDPVIDTC	NSFYCDQFKP	ISNKPMT	ENWNGWADW	GERLPYRPE	299
apple	230	DAPDPVIDTC	NGFYCDNFFP	NKPKPKMT	ENWNGWADW	GERLPYRPE	279
carnation	235	DVDPDIINTC	NGFYCDGFRP	KDKSKPKMT	ENWNGWADW	GERLPYRPE	284
asparagus	231	DAPDPVINTC	NGFYCDYFSP	NKPKPKMT	ENWNGWADW	GERLPYRPE	280
broccoli	231	DAPDPVINTC	NGFYCDYFSP	NKPKPKMT	ENWNGWADW	GERLPYRPE	280
Lupin	239	DAPDPVINTC	NGFYCDNFFP	NKPKPKMT	ENWNGWADW	GERLPYRPE	288
		310	320	330	340	350	
TBG1-ORF	277	DAFAVAREF	OTGGSSEINNY	MYHGGTNEGR	TSCEPMA	GVAVMKOB-	326
TBG2-ORF	287	DAFAVAREF	OTGGSSEINNY	MYHGGTNEGR	TSCEPMA	GVAVMKOB-	336
TBG3-ORF	281	DAFAVAREF	OTGGSSEINNY	MYHGGTNEGR	TSCEPMA	GVAVMKOB-	330
TBG4-ORF	279	DAFAVAREF	OTGGSSEINNY	MYHGGTNEGR	TSCEPMA	GVAVMKOB-	328
TBG5-ORF	301	DAFAVAREF	OTGGSSEINNY	MYHGGTNEGR	TSCEPMA	GVAVMKOB-	350
TBG6-ORF	301	DAFAVAREF	OTGGSSEINNY	MYHGGTNEGR	TSCEPMA	GVAVMKOB-	350
TBG7-ORF	300	DAFAVAREF	OTGGSSEINNY	MYHGGTNEGR	TSCEPMA	GVAVMKOB-	349
apple	280	DAFAVAREF	OTGGSSEINNY	MYHGGTNEGR	TSCEPMA	GVAVMKOB-	329
carnation	285	DAFAVAREF	OTGGSSEINNY	MYHGGTNEGR	TSCEPMA	GVAVMKOB-	334
asparagus	281	DAFAVAREF	OTGGSSEINNY	MYHGGTNEGR	TSCEPMA	GVAVMKOB-	330
broccoli	281	DAFAVAREF	OTGGSSEINNY	MYHGGTNEGR	TSCEPMA	GVAVMKOB-	330
Lupin	289	DAFAVAREF	OTGGSSEINNY	MYHGGTNEGR	TSCEPMA	GVAVMKOB-	338
		360	370	380	390	400	
TBG1-ORF	327	GLRROPKWH	LKDLHRAIKL	CEPALVSD	PAVTSLSGNY	GVAVMKOB-	376
TBG2-ORF	337	GLRROPKWH	LKDLHRAIKL	CEPALVSD	PAVTSLSGNY	GVAVMKOB-	386
TBG3-ORF	331	GLRROPKWH	LKDLHRAIKL	CEPALVSD	PAVTSLSGNY	GVAVMKOB-	380
TBG4-ORF	329	GLRROPKWH	LKDLHRAIKL	CEPALVSD	PAVTSLSGNY	GVAVMKOB-	378
TBG5-ORF	351	GLRROPKWH	LKDLHRAIKL	CEPALVSD	PAVTSLSGNY	GVAVMKOB-	400
TBG6-ORF	351	GLRROPKWH	LKDLHRAIKL	CEPALVSD	PAVTSLSGNY	GVAVMKOB-	400
TBG7-ORF	350	GLRROPKWH	LKDLHRAIKL	CEPALVSD	PAVTSLSGNY	GVAVMKOB-	399
apple	330	GLRROPKWH	LKDLHRAIKL	CEPALVSD	PAVTSLSGNY	GVAVMKOB-	379
carnation	335	GLRROPKWH	LKDLHRAIKL	CEPALVSD	PAVTSLSGNY	GVAVMKOB-	384
asparagus	331	GLRROPKWH	LKDLHRAIKL	CEPALVSD	PAVTSLSGNY	GVAVMKOB-	380
broccoli	331	GLRROPKWH	LKDLHRAIKL	CEPALVSD	PAVTSLSGNY	GVAVMKOB-	380
Lupin	339	GLRROPKWH	LKDLHRAIKL	CEPALVSD	PAVTSLSGNY	GVAVMKOB-	388
		410	420	430	440	450	
TBG1-ORF	377	-----	GACAAFLANY	NOHSFAKVF	GNMHNLPW	SISILPCKN	426
TBG2-ORF	387	NIGQYMSLNE	GICAAFIANI	DEHESATVKF	YGQFTLPPW	SVVF---CQI	436
TBG3-ORF	381	-----	GSCAAFLANY	DQHSFATVSF	ANRHNLPW	SISILPCKN	430
TBG4-ORF	379	-----	GACAAFLSNY	DSRYSVKVT	QNRPNLPW	SISILPCKT	428
TBG5-ORF	401	-----	-----	-----	-----	-----	450
TBG6-ORF	401	-----	-----	-----	-----	-----	450
TBG7-ORF	400	-----	GACAAFLAM	DDKNDKVQF	RHVSYHLPW	SVSILPCKN	449
apple	380	-----	D-CAAFANY	DAKYSVKVSF	GGQYDLPPW	SISILPCKT	429
carnation	385	-----	GSCAAFLANY	DPKYSVKVT	SGMEFELPW	SISILPCKK	434
asparagus	381	-----	-SCAAFLANF	NSRYATVTF	NGMHNLPW	SVSILPCKT	430
broccoli	381	S-----	-SC--FIGNV	NATADALVNF	KGKDYNPW	SVSILPCKT	430
Lupin	389	-----	A-CAAFANY	NTDYSTQVKF	GNGQYDLPPW	SISILPCKT	438
		460	470	480	490	500	
TBG1-ORF	427	TVYNTARVGA	QSAQM--K--	-----	MTP	VSRGFS--WE	476
TBG2-ORF	437	AEIQQLSTQLR	WGHLQSKQW	AQILFQLGII	LCFYKLSLKA	SSESFSQSW	486
TBG3-ORF	431	TVFNTARIGA	QSAQM--K--	-----	MTP	VSRGLP--WQ	480
TBG4-ORF	429	AVYNTAQVNS	QSSSI--K--	-----	MTP	AGGGLS--WQ	478
TBG5-ORF	451	-----	-----	-----	-----	-----	500

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Figure 3
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TBG6-ORF	451	VAFNTAKVGC	OTSIVNMAP	ED	HPTASSE	KRDIKSLONE	499
TBG7-ORF	450	EYVNTAKVGS	OSSQV-Q	MTP	VHSGEF	479	
apple	430	EYVNTAKVNE	PSPKLHSE	MTR	VI SNLN	484	
carnation	435	TUFTIARVGA	OTTTM-K	MOY	LG-GEE	480	
asparagus	431	EAYNTARVNT	QTSIIITDS	-C-	D	EPEKLRWTR	480
broccoli	431	EVFNIAKVNS	PRLHR--K-	MTP	VNSAFA-WO	488	
Lupin	439						
		510	520	530	540	550	
TBG1-ORF	477	S-FNEEAASH	EDD-TSVAVC	MSDOINTTIR	VSDYLWYMID	IELDPTE-CF	526
TBG2-ORF	487	T-LKEPLGW	GDKN-EISKG	IEPHLVVKO	QSDGLWYLR	IYLSDDDISF	536
TBG3-ORF	481	S-FNEETSSY	EDS-SPTVVG	LEDOINTTIR	VSDYLWYSTH	VKIDSRE-KF	530
TBG4-ORF	479	S-YNEETPTA	DDSDILTAG	EWOKNUURE	SSDLXWYMIN	VNTASNE-CF	528
TBG5-ORF	501						550
TBG6-ORF	501						550
TBG7-ORF	500	V-EKETAGWW	GVAL-EIKNG	FVDHEHTKPO	STPDAWTTS	IFVHAEE-DE	549
apple	480	S-ETEEETS	BETITLILDC	LYPOLHIURE	TTHEAWMTTH	ITIGSDH-AF	529
carnation	485	S-YSDEVPTA	DSPGTREERK	LYPOLMIWP	KSGWLWMTD	AVLDGNB-CE	534
asparagus	481	A-YTEDTDAL	NEN-ATKYDG	IVPOLSTWE	RSPHASTTY	VLIADKNE-EE	530
broccoli	481	PERTOKLTIL	KGSGDLIARG	IVDCKOLINE	ASBLHWYTHR	VLHKKKOPIW	530
Lupin	489	S-YNEEPASS	SENDPVGYA	IEWGVGVZRO	SSDWMLTLT	VNTGPNO---	538
		560	570	580	590	600	
TBG1-ORF	527	LNSGN-WBYL	TVFSAGHATH	VEONCOGICE	VVSLE-NRGI	TESNGTNMBA	576
TBG2-ORF	537	WEENDVSRIT	DIDESMRDFVR	IFWACOPAGS	VKRW---I	KVQVPVLSVO	586
TBG3-ORF	531	LRGCK-WBYL	TIMSAGHATH	VFANCOLAGR	AVGSHLKPKT	TFSKAVLRA	580
TBG4-ORF	529	LKNCK-DEYL	TVMSAGHVH	VSNKESGT	VYRTLENFKI	TYSGNVKLEA	578
TBG5-ORF	551						600
TBG6-ORF	551						600
TBG7-ORF	550	LRN-RGTAML	FVESKSHMH	VTINKKHOAS	ASENGTVPOP	KEGTPIAAKA	599
apple	530	LKNCK-SLL	TIFSAGHAIN	VELNGOLSCH	VYESL-NRRI	SRSNNILERS	579
carnation	535	LKTKC-EPYL	TVMSAGHVH	VEANGLOEH	VYSLAKPOE	TSOKWMTA	584
asparagus	531	LKTCK-YPYL	TVMSAGHVH	VELNGOLSCH	AVESLNRKI	TYSGSAKLWA	580
broccoli	531	SRNMS---	RVHSNAHVH	AVANKGVVN	QIVRNKFYD	REEKKVMVH	580
Lupin	539	IKDCK-WBYL	TAMSAGHAIN	VELNGVYASA	VYESLDRRI	TESOSVNLV	588
		610	620	630	640	650	
TBG1-ORF	577	GVNKISLSI	AVGLEPNVGH	FEYNAGVLG	EWSENGINEB	P---RDLTWO	626
TBG2-ORF	587	GVNDILISE	TVGLONYGAF	LEKDGAFFKC	QIKKTECKSC	D---INLTITS	636
TBG3-ORF	581	GVNKISLSI	AVGLEPNVGH	FEYNAGVLG	RWSLGLDBG	K---RDLTWO	630
TBG4-ORF	579	GINKISLSV	SVGLEPNVGH	YDTWNAVIG	PVTLSSLNEG	S---RNLAKQ	628
TBG5-ORF	601						650
TBG6-ORF	601						650
TBG7-ORF	600	GKNEISLSM	TVGLQTAGAF	YE-WIGAGPT	SVKVAGFKTG	T---MDLTAS	649
apple	580	GINKLALLSI	SVGLEPNVGTH	FEYNAGVLG	ETTLKGLNSG	T---WDMSGW	629
carnation	585	GVNRISLSA	SVGLANVGWH	FERYNQGVIG	PVTLSSLNEG	T---RDLTWO	634
asparagus	581	GSNKISLSV	SVGLEPNVNH	FEYNAGVLG	PVTLSSLNEG	K---RDLSLQ	630
broccoli	581	GTNHLALLSV	SVGLQNYGPF	FESGPTGING	EUKLVGYKGD	ETIEKDLSEKH	630
Lupin	589	GNNKISLSV	SVGLANVGTH	FEYNAGVLG	PVTLTGLSSG	T---WDSLKQ	638
		660	670	680	690	700	
TBG1-ORF	627	KWFYKVLKLG	EALSLSLSG	SPSVE--WVE	GSLVAKQOPL	SWYKTTFNAP	676
TBG2-ORF	637	LWTYQVGLRG	EFLEVYDVNS	TESAG--WTE	FPTGITPSVF	SWYKTKFDAP	686
TBG3-ORF	631	KWSYKVLKLG	EALSLSLSG	SSSVE--WVE	GSLVAKQOPL	TWYKSTFNAP	680
TBG4-ORF	629	KWSYKVLKLG	ESLSLSLSG	SSSVE--WVR	GSLMAKQOPL	TWYKATFNAP	678
TBG5-ORF	651						700
TBG6-ORF	651						700
TBG7-ORF	650	AWTYKIGLOG	EHLRIQSYN	LKSKI--WAP	TSOPPQQOPL	TWYKAVVDAP	699
apple	630	KWTYKTGLKG	EALGLHTVTG	SSSVE--WVE	GPSMAEKQPL	TWYKATFNAP	679
carnation	635	YWSYKIGTKG	EBQOVYNSGG	SSHVQ--WGP	PAW---KOPL	VWYKTTFDAP	684
asparagus	631	KWTYQIGLHG	ETLSLSLS				

DNASIS
Multiple Edit1Figure 3
Sheet 4 of 4

TBG2-ORF	687	GCTDPVALDF	SSMGKGOAW	NHIVGRWWT	LVAPN-NGGG	RTGDIRGAFH	736
TBG3-ORF	681	AGNDPLALL	NTMGKGOVWT	NGSLGRWWT	GYKAS-GNCG	A-CNYAGWFT	730
TBG4-ORF	679	GGNDPLALL	ASMGKGOVWT	NSEGVRHWP	GMTAQ-GDCS	K-CSYAGTFN	728
TBG5-ORF	701	-----	-----	-----	-----	-----	750
TBG6-ORF	701	-----	-----	-----	-----	-----	750
TBG7-ORF	700	PGNEPVALIM	IHMKGMAWL	NGEIGRWWT	RRTSKYENCV	TQCDIRGKFN	749
apple	680	PGDAPLALL	GSMGKGOVWT	NGOSVGRHWP	GYIAR-GSCG	D-CSYAGTFD	729
carnation	685	GGNDPLALL	GSMGKGOAWT	NGOSIGRWHS	NNIAK-GSCN	INCNYAGTFY	734
asparagus	681	PGNEPVALIM	NTMGKGOVWT	NGOSIGRWWT	AYKAS-GSCG	S-CDYRGTYN	730
broccoli	681	LKCDPVIVIL	NGLKGEVWT	NGOSIGRWWT	SFNSSDGCT	EEDYRGEYV	730
Lupin	689	AGNDPLALL	GSMGKGEVWT	NGOSIGRHWP	GNKAR-GNCG	N-CNYAGTFY	738
TBG1-ORF	727	EKKCLTNGGE	GSORWYHVP	SMYPTGNLL	V-VFEENGCD	PYGITLVKRE	776
TBG2-ORF	737	SDKCRTHNGE	ITQAWYHPR	SMYKTLANVL	V-IFFEETDKT	PFDKSISTRS	786
TBG3-ORF	731	EKKCLSNNGE	ASORWYHVP	SMYPTGNLL	V-LFEENGGE	PHGSLVKRE	780
TBG4-ORF	729	EKKCOIVNGO	ESORWYHVP	SMYKPSGILL	V-VFEENGCD	ETGSLVKRS	778
TBG5-ORF	751	-----	-----	-----	-----	-----	800
TBG6-ORF	751	-----	-----	-----	-----	-----	800
TBG7-ORF	750	PDKCVTHNGO	PTORWYHVP	SMYKPSGIVL	I-IFFEETDKT	ESDRFSMEK	799
apple	730	DKKCRTHNGE	ESORWYHPR	SMYPTGNLL	V-VFEENGCD	ESRISVVERG	779
carnation	735	EKKCLSDGCK	SSORWYHVP	SMYDPRGNGE	V-VFEENGCD	TKWVSLVKRT	784
asparagus	731	EKKCLSNNGE	ASORWYHVP	SMYPTGNLL	V-LFEENGGE	ETGSLVKRS	780
broccoli	731	SDKCAFMECK	PTORWYHVP	SFINDKCHNT	ITLFEENGCD	ESMVKFTVV	780
Lupin	739	DTKCLANNGO	ESORWYHVP	SMYKPSGIVL	V-VFEENGCD	ENGSLVKRT	788
TBG1-ORF	777	IGSVCAEVEE	NG-POLVNM	RLVSKFDRK	NR-PRKHLK	GAPGOKLSSA	826
TBG2-ORF	787	TETICAOVSE	KHYRPLHKNS	HSEFDRKLSL	MDKTPPMHIO	GDEGHTESST	836
TBG3-ORF	781	VASVCADINE	NG-POLVNM	MOASCKVDRK	NR-PRKHLK	GASGOKLSSA	830
TBG4-ORF	779	-----	-----	-----	-----	-----	828
TBG5-ORF	801	-----	-----	-----	-----	-----	850
TBG6-ORF	801	-----	-----	-----	-----	-----	850
TBG7-ORF	800	VSGACGHLV	-DHESFD-V	ENLQSEIEN	DKNRPTLSLK	CPTNINISSV	849
apple	780	IA-	-----	-----	TA	ND-AK	829
carnation	785	IA-	-----	-----	-----	-----	834
asparagus	781	VASVCAVEVE	LQ-PIMINVR	TKBYG	-R-PKVHLS	CDGOKMSKI	830
broccoli	781	TGRVCAKAHE	-----	-----	-----	HNKVELS	830
Lupin	789	-----	-----	-----	-----	GN-NRPTISAV	838
TBG1-ORF	827	KFASFGTPEG	VCGNFOGSGC	HAPRSYDAFK	K-----NCVG	KESCSVQVTP	876
TBG2-ORF	837	EFASYGSPNG	SCOKESOGKC	HAANLSV--	---VSQACIG	RTSCSIGISN	886
TBG3-ORF	831	KFASFGTPOG	VCGSFREGSC	HAFHSYDAFE	R-----YCIG	QNSCSVPVTP	880
TBG4-ORF	829	-----	-----	-----	-----	-----	878
TBG5-ORF	851	-----	-----	-----	-----	-----	900
TBG6-ORF	851	-----	-----	-----	-----	-----	900
TBG7-ORF	850	KFASFGNPNG	TCGSYMLGDC	HDQNSAALVE	K-----VCLN	QNECALEMSS	899
apple	830	-----	-----	-----	-----	-----	879
carnation	835	-----	-----	-----	-----	-----	884
asparagus	831	KFASFGTPOG	TCGSFSEGSC	HAHKSYDAFE	QEGLMQNCVG	QEFCSVNAP	880
broccoli	831	KFASFGNPSG	QCGSFAAGSC	EGAKDAVKV-	---VAKECVG	KLNCTMNVSS	880
Lupin	839	-----	-----	-----	-----	-----	888
TBG1-ORF	877	ENFGGDP-CR	NVLKKLSVEA	ICS-----	-----	-----	926
TBG2-ORF	887	GVFG-DP-CR	HVVKSLAVQA	KCSPPDLST	SASS.....	-----	936
TBG3-ORF	881	EI FGGDP-CP	HVMKKLSVEV	ICS-----	-----	-----	930
TBG4-ORF	879	-----	-----	-----	-----	-----	928
TBG5-ORF	901	-----	-----	-----	-----	-----	950
TBG6-ORF	901	-----	-----	-----	-----	-----	950
TBG7-ORF	900	ANFNMQL-CP	STVKKLAVEV	NCS-----	-----	-----	949
apple	880	-----	KL-----	-----	-----	-----	929
carnation	885	-----	-----	-----	-----	-----	934
asparagus	881	EVFGGDP-CP	GTMKKLAVEA	ICE-----	-----	-----	930
broccoli	881	HKFGSNLDCG	DSPKRLFVEV	EC-----	-----	-----	930

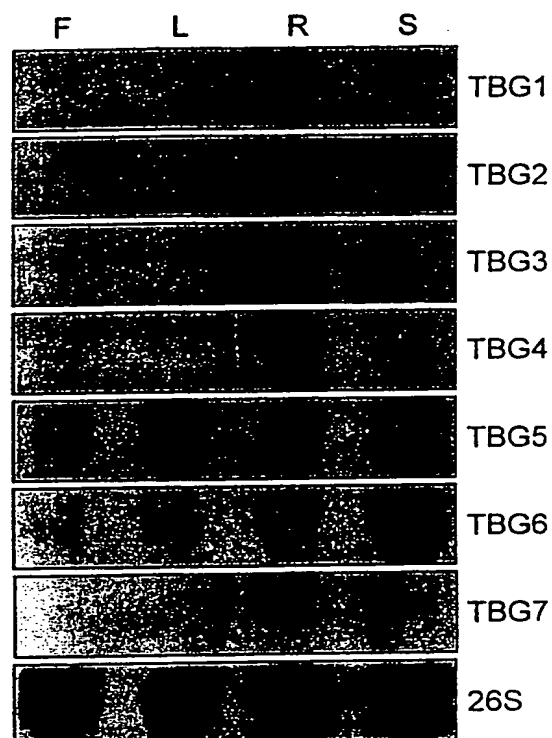


Figure 4. Autoradiograph of northern blot analysis of TBG expression in various plant tissues. Twenty μg of total RNA extracted from flowers (F), leaves (L), roots (R) and stems (S) was loaded in each lane. RNAs were separated in an agarose gel and transferred to nylon membrane. Blots were hybridized using the probes indicated to the right, washed to a final stringency of 0.1X SSC at 65°C and were used to expose x-ray film. A 26S ribosomal gene clone from soybean was used as a loading control for each blot and one example is shown.

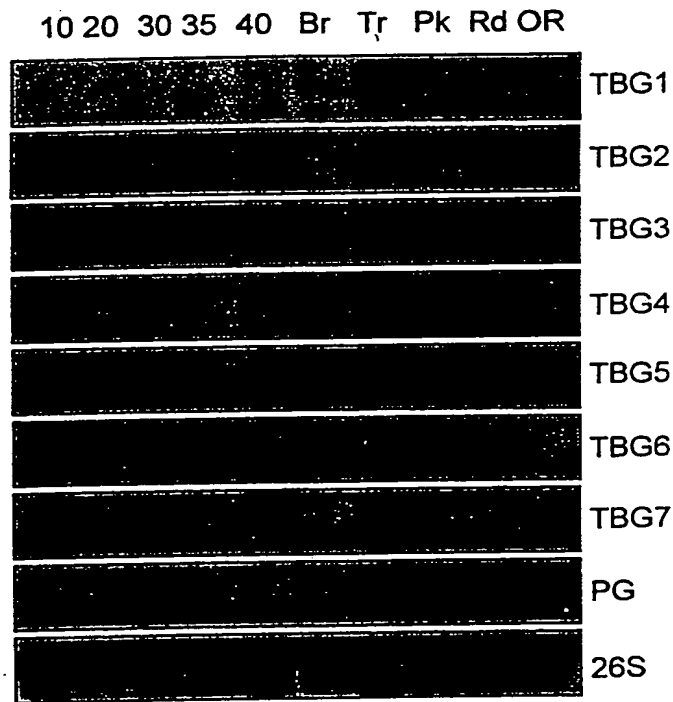


Figure 5. Autoradiograph of northern blot analysis of TBG expression in fruit tissues. Twenty μ g of total RNA extracted from peel and outer pericarp tissue was loaded in each lane. Fruit were harvested at 10, 20, 30, 35, and 40 days post-pollination and at the breaker (Br), turning (Tr), pink (Pk), red (Rd) and over ripe (OR) stages. RNAs were separated in an agarose gel and transferred to nylon membrane. Blots were hybridized using the probes indicated to the right, washed to a final stringency of 0.1X SSC at 65°C and were used to expose x-ray film. A 26S ribosomal gene clone from soybean was used as a loading control for each blot and one example is shown. A cDNA clone for tomato polygalacturonase (PG) was also used as a probe to show a well characterized, fruit-ripening-specific control.

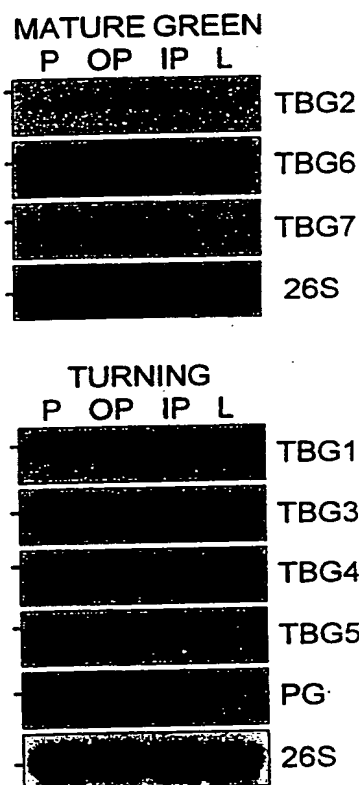


Figure 6. Autoradiograph of northern blot analysis of TBG expression in fruit tissues. Twenty μ g of total RNA extracted from mature green or turning stage fruit peel (P), outer pericarp (OP), inner pericarp (IP) and locular (L) tissue was loaded in each lane. RNAs were separated in an agarose gel and transferred to nylon membrane. Blots were hybridized using the probes indicated to the right, washed to a final stringency of 0.1X SSC at 65°C and were used to expose x-ray film. A 26S ribosomal gene clone from soybean was used as a loading control for each blot and one example is shown. A cDNA clone for tomato polygalacturonase (PG) was also used as a probe to show a well characterized, fruit-ripening-specific control.

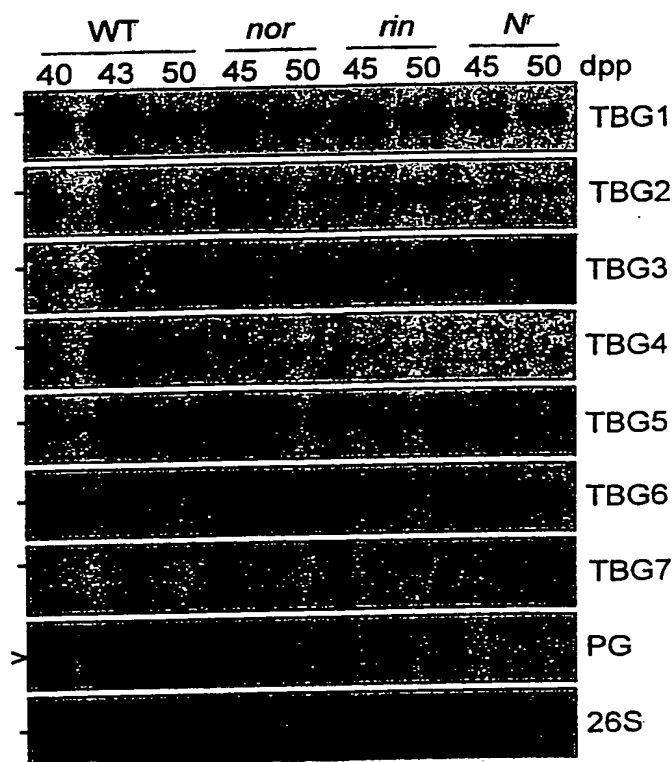


Figure 7. Autoradiograph of northern blot analysis of TBG expression in normal and mutant fruit tissues. Twenty μ g of total RNA extracted from peel and outer pericarp tissue at various days post-pollination (dpp) was loaded in each lane. RNAs were separated in an agarose gel and transferred to nylon membrane. Blots were hybridized using the probes indicated to the right, washed to a final stringency of 0.1X SSC at 65°C and were used to expose x-ray film. A 26S ribosomal gene clone from soybean was used as a loading control for each blot and one example is shown. A cDNA clone for tomato polygalacturonase (PG) was also used as a probe to show a well characterized, fruit-ripening-specific control. The - and > marks on the left indicate the position of the tomato 27S and 18S rRNAs respectively.

0000 0000 0000 0000 0000 0000 0000 0000

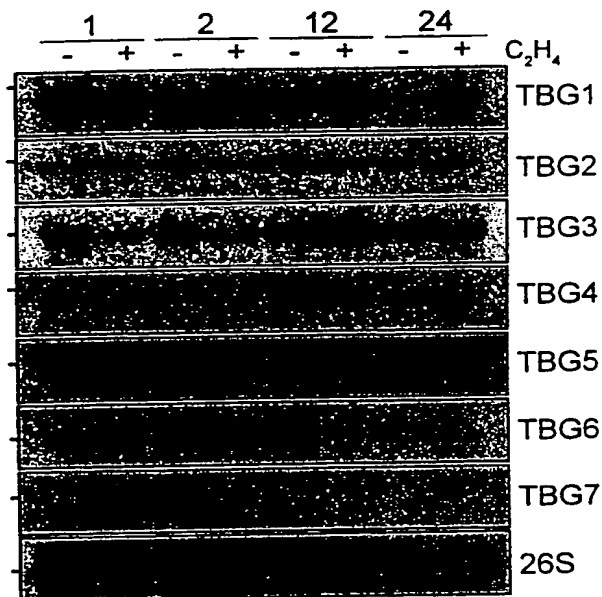


Figure 8. Autoradiograph of northern blot analysis of TBG expression in response to ethylene treatment of mature green fruit tissues. Twenty μ g of total RNA extracted from peel and outer pericarp tissue at various times (1, 2, 12 and 24 hours) after treatment with (+) or without (-) 10 ppm ethylene was loaded in each lane. RNAs were separated in an agarose gel and transferred to nylon membrane. Blots were hybridized using the probes indicated to the right, washed to a final stringency of 0.1X SSC at 65°C and were used to expose x-ray film. A 26S ribosomal gene clone from soybean was used as a loading control for each blot and one example is shown. The - marks on the left indicate the position of the tomato 27S rRNA.



Figure 9. Western blot analysis of TBG4 expression by yeast. A yeast clone was isolated that secreted high levels of FLAG-TBG4 fusion protein into the culture medium. Protein samples were separated in an 8% acrylamide gel, transferred to nitrocellulose and were blotted with M1 anti-FLAG primary antibody. Blots were washed and blotted with an alkaline-phosphatase conjugated secondary antibody and alkaline phosphatase activity was detected using Sigma Fast substrate. Lane 1, culture medium of an untransformed yeast clone was used as a negative control. Lane 2, culture medium of yeast clone expressing FLAG-TBG4 fusion protein. Lane 3, Affinity purified FLAG-TBG4 fusion protein.

Figure 10

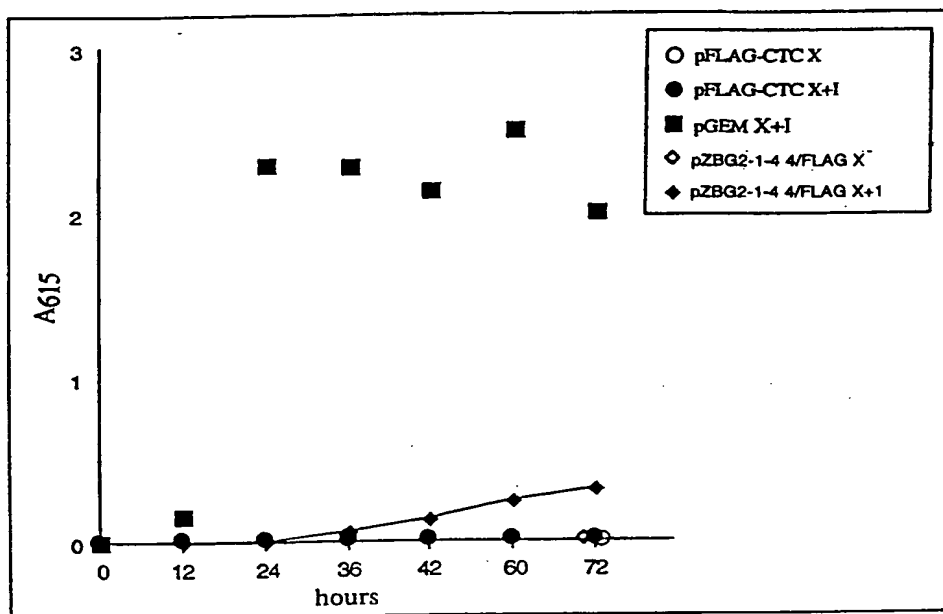
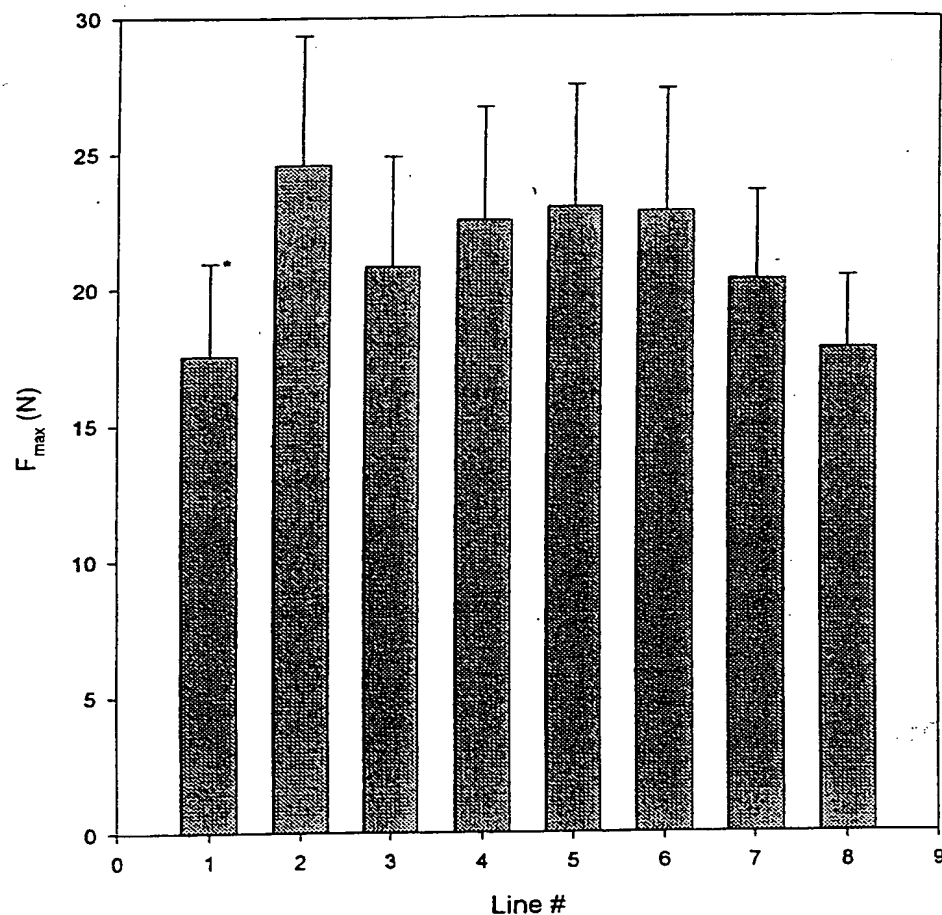


Figure 11A

Flat plate compression to 3 mm
Breaker + 7 d



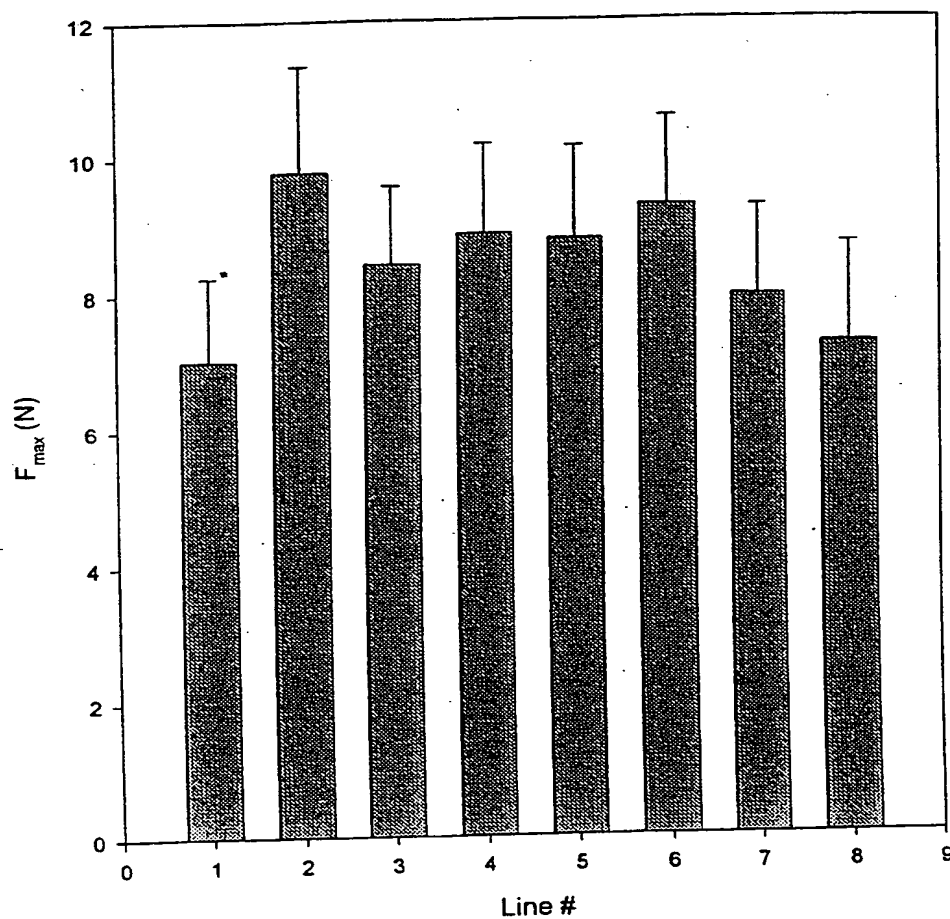
* Standard Deviation

FP07 Line # FP07 mean FP07 std dev

1	17.52665	3.418542
2	24.56026	4.786548
3	20.81681	4.066194
4	22.54655	4.15923
5	23.03255	4.493091
6	22.84338	4.517462
7	20.36124	3.24608
8	17.81924	2.665468

Figure 11B

Spherical indenter to 3 mm
Breaker + 7 d

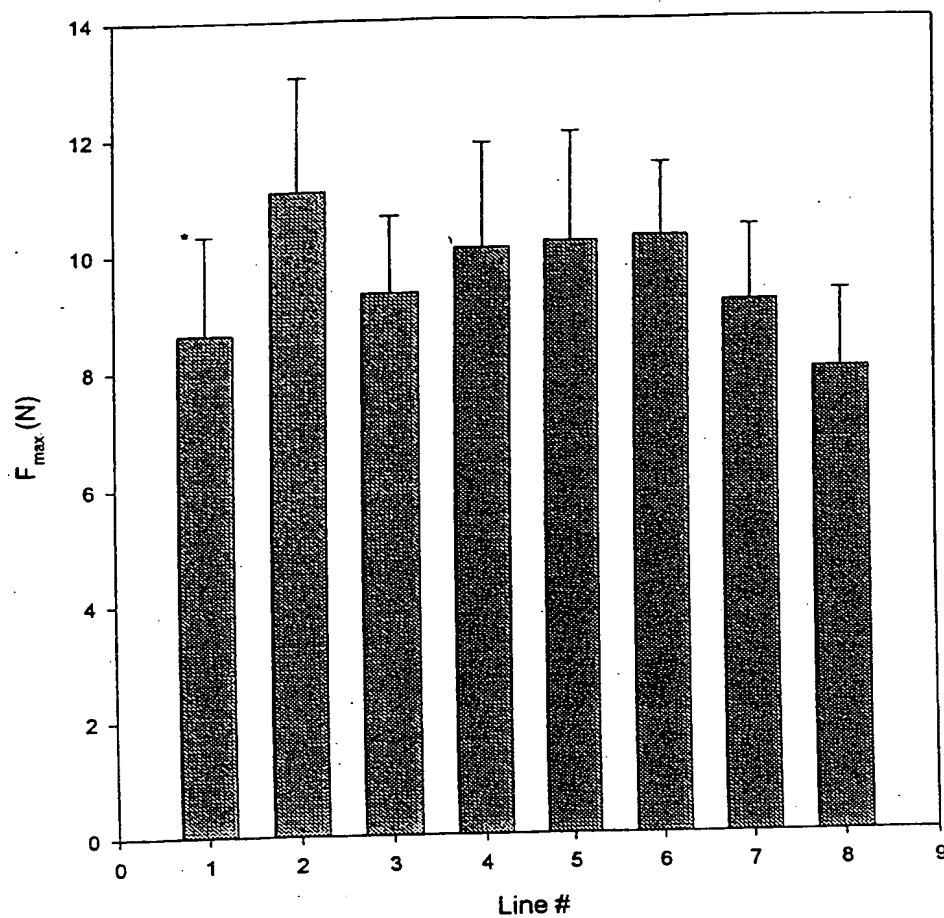


* Standard Deviation

SP07 Line #	SP07 Mean	SP07 Std Dev
1	7.02	1.22
5	9.77	1.57
6	8.43	1.15
7	8.87	1.32
8	8.78	1.36
9	9.28	1.29
11	7.96	1.30
12	7.26	1.45

Figure 11C

4-mm cylindrical indenter to 1 mm
Breaker + 7 d

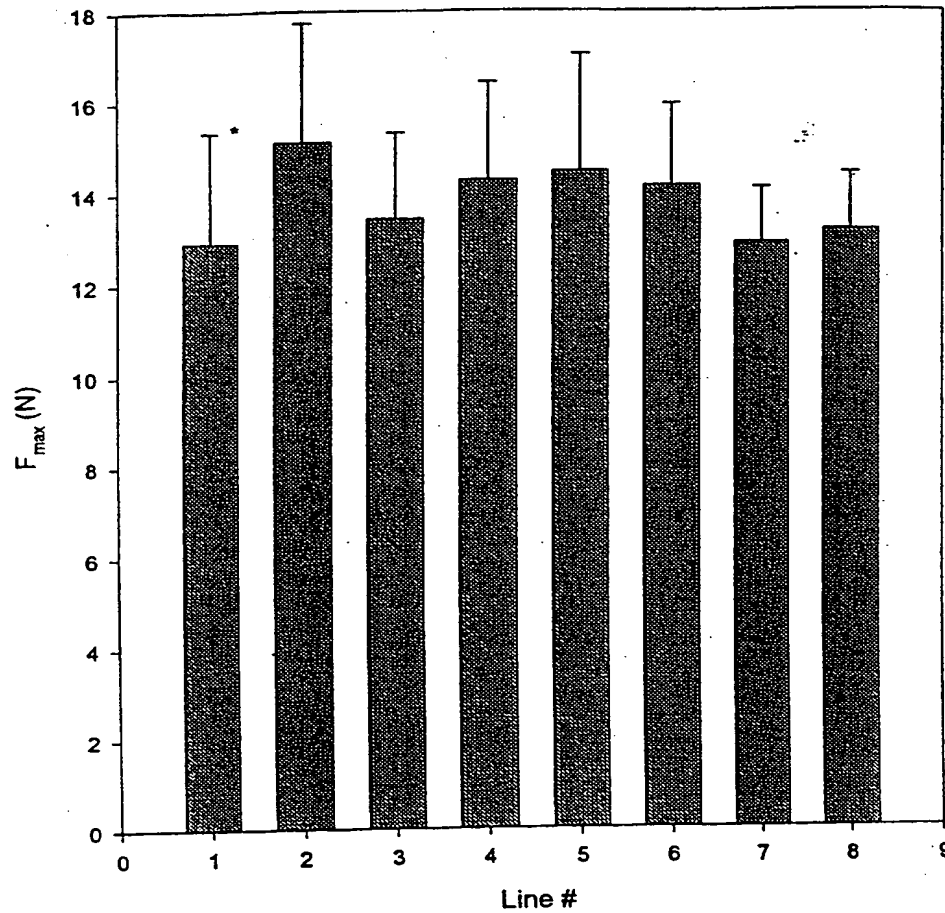


• Standard Deviation

CY07 LINE#	CY07 Mean	CY07 Std Dev
1	8.62	1.69
5	11.07	1.96
6	9.31	1.33
7	10.07	1.81
8	10.18	1.88
9	10.27	1.26
11	9.15	1.30
12	7.99	1.33

Figure 11D

4-mm cylindrical puncture to 1 mm
Breaker + 7.8



* Standard Deviation

PU07 Line#	PU07 Mean	PU07 Std Dev
1	12.91	2.43
5	15.13	2.61
6	13.44	1.90
7	14.28	2.16
8	14.47	2.58
9	14.14	1.81
11	12.90	1.20
12	13.18	1.25

FIG. 11 E (1)
Flat plate compression to 3 mm
Breaker + 7 d

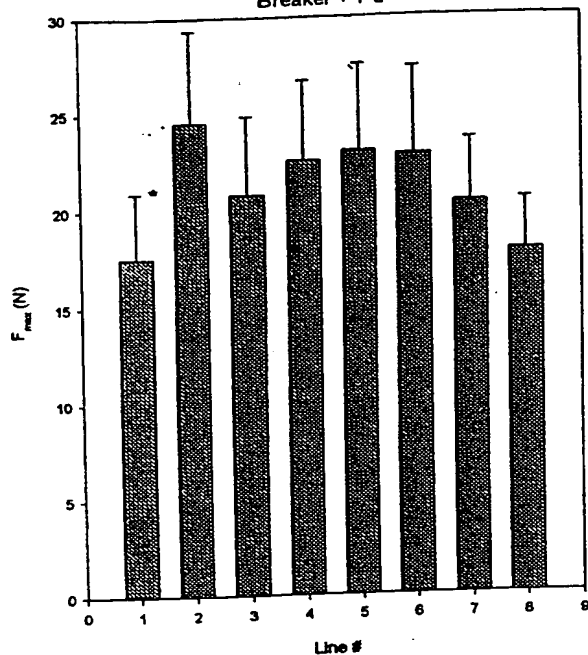


FIG. 11 E (2)
Spherical indenter to 3 mm
Breaker + 7 d

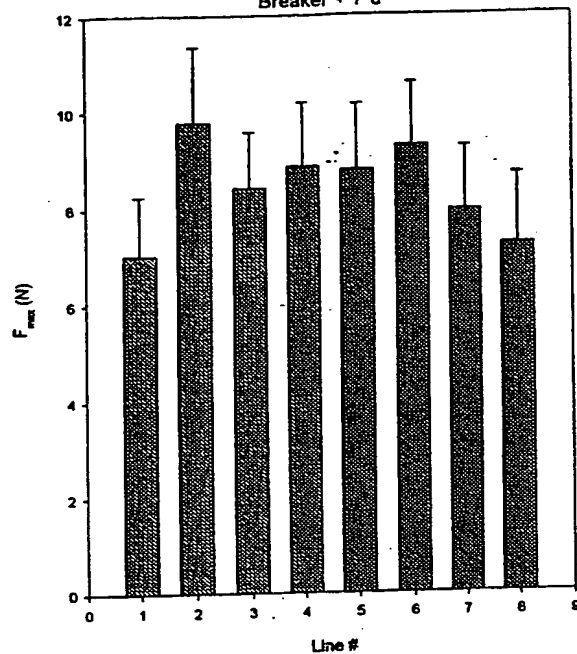


FIG. 11 E (3)
4-mm cylindrical indenter to 3 mm
Breaker + 7 d

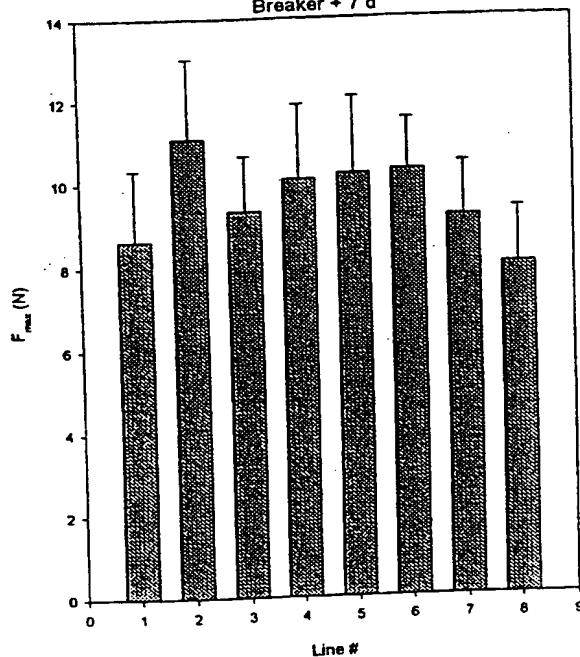
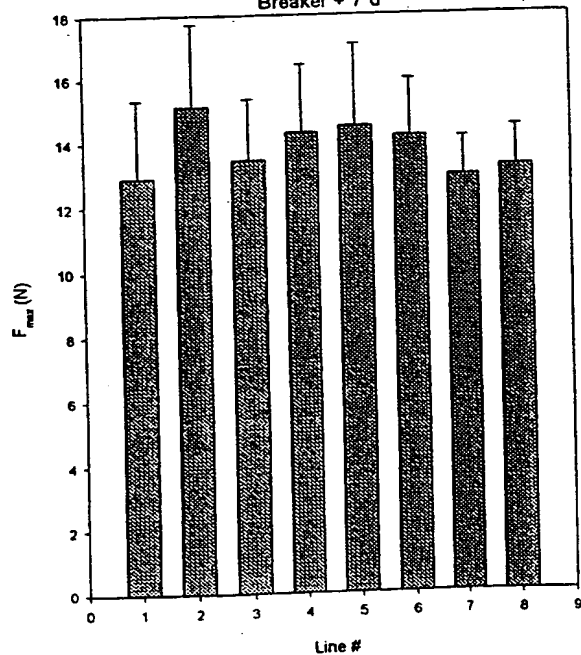


FIG. 11 E (4)
4-mm cylindrical puncture to 10 mm
Breaker + 7 d



* Standard Deviation

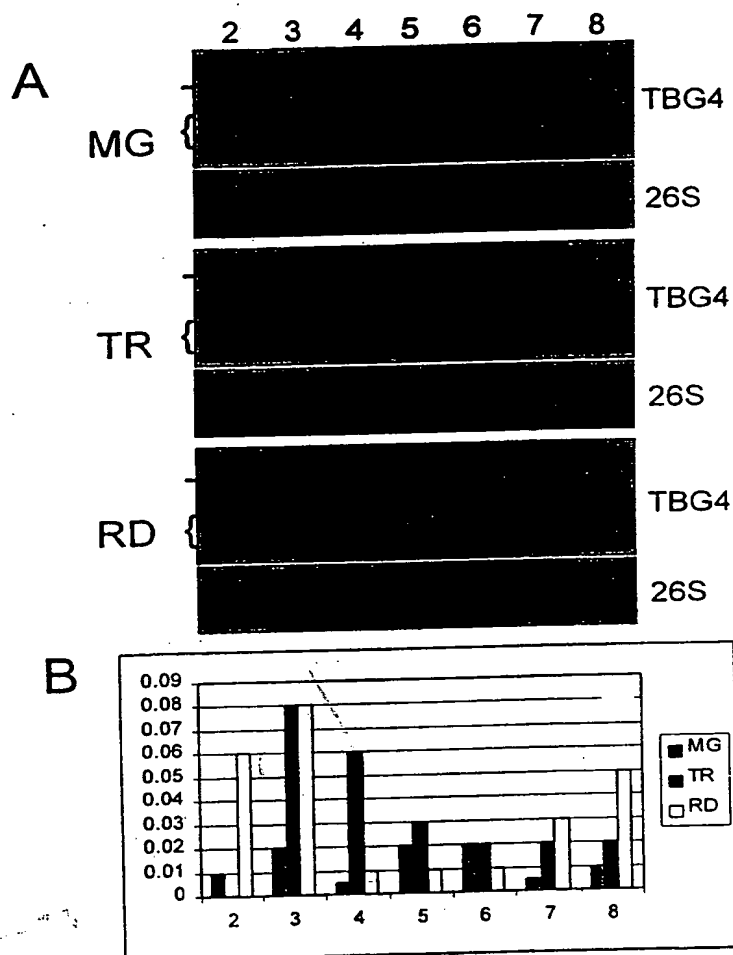


Figure 12. Northern blot analysis of TBG4 expression in transgenic fruit containing TBG4 antisense construct. A. Total RNA was extracted from mature green/42 days post-pollination (MG), turning/breaker + 3 (TR) and red/breaker + 7 (RD) fruit and twenty μ g was loaded in each lane. RNAs were separated in an agarose gel and transferred to nylon membrane. Blots were hybridized using the probes indicated to the right, washed to a final stringency of 0.1X SSC at 65°C and were used to expose x-ray film. A 26S ribosomal gene clone from soybean was used as a loading control. The marks - and { denote the positions of the endogenous TBG4 and antisense mRNAs respectively. Lanes 2-8 correspond to transgenic lines 2-8 in Figures 11A-E. B. Chart of TBG4 mRNA levels in lines 2-8. Autoradiographs were scanned using a densitometer and TBG4 mRNA levels were corrected against the loading controls. TBG4 mRNA levels are shown in arbitrary units.

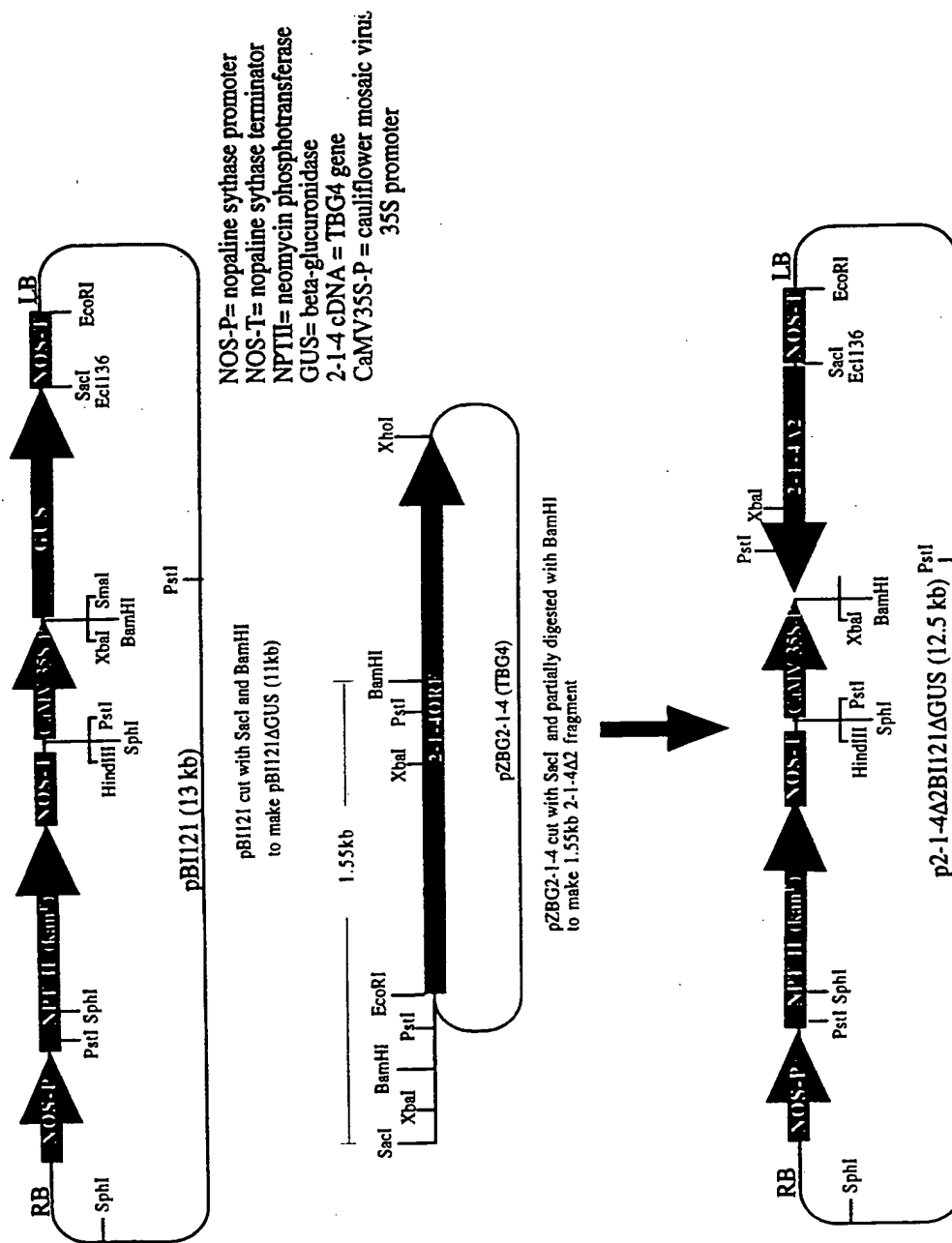


Figure 13. Binary construct used to transform plants and express TBG4 (pZBG2-1-4) in the antisense orientation.